Title: Perfect score: Sequence:

US-09-104-340-4 1466 1 MDCQLSILLLLSCS

OM protein

protein search, using sw model

GenCore version Copyright (c) 1993 - 2000

4.5 Compugen

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Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Issued_Patents_AA:*
1: /cgn2_6/ptodata/;
2: /cgn2_6/ptodata/;
3: /cgn2_6/ptodata/;
4: /cgn2_6/ptodata/;
5: /cgn2_6/ptodata/

Minimum DB Maximum DB

seq

length: 0 length: 1000000

Total number of hits satisfying chosen parameters:

143561 seqs, 14463640 residues

Searched:

5, Appli 12, Appli 11, Appli 11, Appli 11, Appli 11, Appli 6, Appli 6, Appli 20, Appli

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/iaa/COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Sequence 21,
Sequence 10,
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               Sequence
   e 21, Apple 22, Apple 22, Apple 22, Apple 23, Apple 23, Apple 23, Apple 23, Apple 23, Apple 24, Apple 24, Apple 25, 
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; Patent No.
; GENERAL IN
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1C
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,919A
FILING DATE: 18-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION UNMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PCT/AU92/00294
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGITION STATE

APPLICATION PAPELORY

APPLICATION PAPELORY

APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RI
TITLE OF INVENTION: AND USE TI
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444333543310
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CITY: G
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5. 5674691
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T: 400 Garden City Plaza
Garden City
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US-08-162-809-12
US-08-162-809-12
US-08-449-645A-11
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Result No.

Score

Query Match

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SUMMARIES

US-08-167-919A-10
US-08-449-645A-21
US-08-715-106-10
PCT-US95-04681-21
US-08-673-789-4
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PCT-US95-04681-17

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; TOPOLOGY: 11;
; MOLECULE TYPE:
US-08-449-645A-21
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                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERRINCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             veywence 21, Application US/08449645A Patent No. 5981245
                                                                            Query Match
Best Local Similarity
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Best Local :
                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-LIKE
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Amgen Patent Operations/RBW STREET: 1840 Dehavilland Drive CITY: Thousand Oaks STATE: California
                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60
1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60
              MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60
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MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP
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                                                           Score 1466;
Pred. No. 5.2
0; Mismatches
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Pred. No. 5.2e-146;
Mismatches 0;
                                                           DB 2;
5.2e-146;
es 0;
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Best Local S
Matches 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOCOMPATION FOR PROPERTIES
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
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STATE: California
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: EPH-Like
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                                                                                                                    HYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETF 120
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 LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP
                                                 NLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFY 180
                                                                                                HYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETF 120
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5. 5981246
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1840 Dehavilland Drive
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Pred. No. 5.2e-146;
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TELEPAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEO ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
                                                              Query Match
Best Local Similarity
Matches 271; Conserv
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EILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
EILING DATE: 19-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: D1G19110, FIRM S.
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                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK.841 (AU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-JUN-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE
TITLE OF INVENTION: AND USE THEREOF
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ZIP: 11530
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MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60
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llarity 100.0%;
Conservative (
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                                                                   Score 1466; DB 3;
Pred. No. 5.2e-146;
; Mismatches 0;
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04681-21
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PCT-US95-04681-21
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Matches 271; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
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181
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CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                                     1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60
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                                                              NLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFY
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Pred. No. 5.2e-146;
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US-08-162-809-16
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; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-162-809-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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Best Local Similarity

Matches 240; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4370 La Jolla VII
CITY: San Diego
STATE: California
COUNTRY: United States of
ZIP: 92122
COMPTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS COMMERCES SEQUENCES. 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                EWLVPIGKCSCNAGYEERGFMCQ 271
                                                                             CVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG
                                                                                                                      DDHLAKFREHQFTKIDTMAADESFTQMDLGDRILKLNTEVREVGPVSKKGFYLAFQDVGA
                                                                                                                                        DDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGA 188
                                                                                                                                                                                  LLLCAALGSAGRLSARPGNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTY
                                                                                                                                                                                                                                                                   LLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTY 68
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EWLVPIGKCLCNAGYEERGFACQ
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                                                                                                                                                                                                                                                                                                               Score 1306; DB 1; Length 983; Pred. No. 4e-129; 9; Mismatches 14; Indels
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Best Local S
Matches 240
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                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,34
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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248
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                                                   188
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                                                                                                       128
                                                                                                                                  129
                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID
STRANDEDNESS: UNI
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                        CVALVSVRVYFKKCPFTVKNLAMFDDTVPMDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG 248
                                                                                                   EWLVPIGKCLCNAGYEERGFACQ 270
                       EWLVPIGKCSCNAGYEERGFMCQ 271
                                                  CVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNHSKEEEPPKMYCSTEG
                                                                                                                                                                                                                                                                    Similarity 91.:
40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZHOU,
                                                                                                                                                                                                                                                                                                                                                    UNKNOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOU, RENPING; SCHULZ, NICHOLAS, KROMER, LAWRENCE, F.; VANDE
                                                                                                                                                                                                                                                                                                                                                                 UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BSK RECEPTOR LIKE
TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
                                                                                                                                                                                                                                                                                88.8%;
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                                                                                                                                                                                                                                                                                Score 1302; DB 2;
Pred. No. 1e-128;
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US-08-673-789-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/177,81

FILING DATE: 04-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026

TELEPHONE: (212) 758-4800

TELEPHONE: (212) 758-6849

TELEYX: 421792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBI
OPERATING SYSTEM: PC-DOS/N
SOFTWARE: WORDDERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ZHOU, RENFING; SCHULZ, NICHOLAS, APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE, APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPE TITLE OF INVENTION: METHODS
                                                                                                                         147
 267
                                                              207
                                                                                                                                                        145
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                                                                                                                                                                                                                      85
                                                                                                                                                                                                                                                                  26 PSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT 84
                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: UNI
                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/673,789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                    TIAADESFTOMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF 204
                                                                                                                                                                                                   NWYPRNSAQKIYYELKFTLRDCNSIPLYLGTCKETFNLYYMESDDDHGYKFREHQFTKID 144
                                                         EERGFMCQ
                                                                                                                                                                                                                                                  PANEVILLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMEASQNNWLRT 86
                                                                              TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGY 263
 EERGFACQ
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274
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                                                                                                                                                                                                                                                                                                           68.6%; Score 1005; DB 2; 73.0%; Pred. No. 2.2e-97; tive 33; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BSK RECEPTOR LIKE
TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
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; STRANDEDNESS:
; TOPOLOGY: unkr
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US-08-469-537A-101
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US-08-469-537A-101
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                                                                                                                                                                                                                                                                                                    Query Match 68.4%; Score 1003; DB 2; Best Local Similarity 65.7%; Pred. No. 3.4e-97; Matches 180; Conservative 39; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECHOME: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Maisonpierre, et
TITLE OF INVENTION: EHK AND
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 948 amino acid
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                                 177
                                                                   173
232 NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                                                TELEPHONE: 914-345-74
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Regeneron Pharmaceuticals, STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                   LGTCKETFTLYXIESDESHGTKFKPSQXIKIDTIAADESFTQMDLGDRILKLNTEVREVG
                                                                                                                       LGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVG 172
                                 PIERKGFYLAFQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCV
                                                   PVNKKGEYLAFQDVGACVALVSVRYYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01, Application 5843749
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                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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                                                                                                                                                                                                                                                                                                                                    Length 948;
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237

270

TITLE OF INVENTION:

Kinases

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RESULT 11
US-08-702-367A-15
US-08-702-367A-15
; Sequence 15, Application U;
; Patent No. 5981246
; Patent INFORMATION:
; APPLICANT: FOX, GATY M
; TITLE OF INVENTION: EP;
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US-08-449-645A-15
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application Patent No. 5981245 GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                   GACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSCVNNSEEKDVPKMYCG
                                                                                                                                                                                                                                    GACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCS
                                                                                                                                                                                                                                                                               SUNDKERFIRENGFVKIDTIAADESFTGVDIGDRIMKLNTEIRDVGPLSKKGFYLAFQDV
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EPH-Like Receptor Protein
                                                                    US/08702367A
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 Tyrosine
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-367A-15
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                                                                                                                                                                                                                                           Sequence 15, Application PC/TUS9504681 GENERAL INFORMATION:
APPLICANT: FOX, GATY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 183;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367
                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         APPLICANT: FOX, Gary M.
TITLE OF INVENTION: EPH-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                           COUNTRY: U
                                                                                            ADDRESSEE: Angen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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STATE: California
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 TYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPGVMGTCKETFNLYYYE 128
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1840 Dehavilland Drive
                                                                               USA
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Pred. No. 2.5e-96;
7; Mismatches 42
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US-08-222-616-36
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ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/08222616 Patent No. 5635177
                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.9%;
Best Local Similarity 68.8%;
            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb fl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/222,616
FILING DATE: 4-APR.1994
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                         APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                               STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCS 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDV 186
                                                                                                                                                                 USA
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                               US/08/222,616
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                                                                                                               360 Kb floppy disk
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Pred. No. 2.5e-96;
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PCT-US95-04228-36
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TELEPHONE: 415/225-1994
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Applicat
GENERAL INFORMATION:
APPLICANT: Genent
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Best Local Similarity 68.8%; Pred. No. 3e-96;
Matches 183; Conservative 37; Mismatches
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 K
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                   APPLICANT: Tsai, S:
APPLICANT: Wood, W:
TITLE OF INVENTION:
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129
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                                                                                                            COUNTRY:
ZIP: 940
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                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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REFERENCE/DOCKET NUMBER:
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WOOD, WILLIAM I.
WENTION: POTEIN TYROSINE KINASE AGONIST ANTIBODIES
                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                             Bennett, Brian
Goeddel, David
                                                                                                                                                                                                                                                                                                         Lee, James M.
Matthews, William
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FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00.000
REFERENCE/DOCKET NUMBER: 821P:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-1994
TELEFAX: 415/952-9881
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Best Local Similarity 68.8%; Pred. No. 3e-96;
                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08673789 Patent No. 5814479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 183;
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                       APPLICANT: T.; KROMER, LAWRENCE, APPLICANT: GEORGE, F. TITLE OF INVENTION: BSK RECEPTOR TITLE OF INVENTION: TYROSINE KING TITLE OF INVENTION: WETHODS
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                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
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ADGEWLVPIGNCLCNAGHEERSGECQ 274
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                                                                                                      USA
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TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
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Search completed: May Job time: 4151 sec

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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/177,81:
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (217) 751-6849
TELEFX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
I ENURTH. 8377
                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.5%; Score 990; DB 2; Best Local Similarity 66.2%; Pred. No. 7.2e-96; Matches 174; Conservative 44; Mismatches 41
 283
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                                                                                            190 VALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG 248
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TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
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                                                                                                                                                                                                                                              70 VCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIFLVLGTCKETFNLYYMESDD 129
                                                                                                                                                                                                                                                                                                                       10 LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ 69
                                                                        VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD 162
EWLVPIGKCMCKAGYEEKNGTCQ 305
                                     EWLVPIGKCSCNAGYEERGFMCQ 271
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: мау 9, 2000, 21:52:05; Search time 50.71 Seconds (without alignments) 126.581 Million cell updates/sec

Title: Perfect score: Sequence: US-09-104-340-4
1466
1 MDCQLSILLLSCSVLDSFG......VPIGKCSCNAGYEERGEMCQ 271

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 188963 segs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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or ien	P-PSDB; R31466. Receptor-type tyrosine kinase reactive with monoclonal antibody III-A4 - is EPH-ELK-like kinase, useful for phosphorylating proteins in modulating pre-B, B and T cell function, in cancer therapy etc.		/note= "ATP binding site" modified_site 779 /note= "Putative autophosphorylation site" M09300425-A.	/note= "ATP _site 630 /note= "ATP _site 633	<pre>/note= "N-link glycosylation" domain 542565 /note= "Transmembrane domain" binding_site 628</pre>	393 "N-link 406 "N-link 495	860 "Purified HEK 234 "N-link glycos 339 "N-link glycos	n e aprene	T 1 6 6 R3146 R3146 Prime Prime Prime Prime

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Gallus sp.
WO9515375-A.
08-JUN-1995.
                                                                                                                                                      Disclosure; Page 85-89; 129pp; English.

Probes derived from the EPH-related PTKs Cek4 (Q90659) and Ce (Q90660) were used to isolate novel cDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues and also in the adult brain and retina. Sequence 983 AA;
                                                                                                                                                                                                                                                   07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RES
PASQUALE EB, SAJJAdi FG;
WPI; 95-215255/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production and/or function analogues have activity in cellular responses such as Sequence 983 AA;
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R75711;
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                                                                                                                                                                                                                           cancer.
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DDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGFVNKKGFYLAFQDVGA
                            LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of pre-B, B and T cells. The TK and transducing signals or in stimulating growth and/or differentiation.
                                                                                                        9; Mismatches
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Pred.
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No. 6.5e-143;
                                                                                                                                                                                                                                                                                                                                          PTK;
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                                                                                                                 DB
.3e-1
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                                                                                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                  monitoring
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                                                                                                                                                                                                                                                                                                                                          diagnosis;
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RESULT
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Best Local S
Matches 180
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17-MAR-1995; US-406247.
26-JUL-1991; US-736559.
28-OCT-1993; US-144992.
06-JUN-1995; US-469537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       il-FEB-1999 (first entry)
Rat receptor tyrosine kinase Ehk-2.
Receptor tyrosine kinase; Ror-1; Ro
neurotrophin activity; trkB; proto-
binding protein; BDNF; NT-3; diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 21; 194pp; English.

The present invention describes nucleic acid molecules for ror-1 ror-2, ehk-1 and ehk-2. Also described are the corresponding pro Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence represents rat Ehk-2. Sequence 948 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGE-) REGENERON PHARM INC.
Maisonplerre PC, Masiakowski
WPI; 99-044584/04.
N-PSDB; V70208.
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US5843749-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding receptor tyrosine kinase
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                                                                                                                                                                                                                                                                                                                                                                                   LGTCKETFTLYXIESDESHGTKFKPSQXIKIDTIAADESFTQMDLGDRILKLNTEVREVG
                                                                                                                                                                                                                                                                                                                                                                                                            LGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVG
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                                                                                                                                                                                          KSSEERDTPKLYCGADGDWLVPLGRCICTTGYEE
                                                                                                                                                                                                                                          NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                                                                                                                                                                       PIERKGFYLAFQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCV
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proto-oncogene; tyrosine kinase receptor;
diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.6e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270
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R85936 stand R85936; 14-FEB-1996

standard;

Protein;

986

8

Protein tyrosine-kinase

bpTK7

(first

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RESULT
R85091
R85091
R10
AC R10
DT 11
DE E1
DE E1
DE E1
PN H10
PN H10
PN H10
PR 11
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Best Loca
Matches
                          Homo sapiens.
W09528484-A1.
26-OCT-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T03100.

Agonist antibodies which activate specific protein tyrosine Agonist antibodies which activate proteins of kinase extracellular kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic modulation of, cell growth and differentiation modulation of, cell growth and differentiation Disclosure; Page 95-99; 125pp; English.

DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify novel pTK genes. The bpTKs, bpTK1, bpTK2, bpTK3, bpTK4, bpTK5 and bpTK7 (R85924-28 and R85935, respectively) are expressed in human brain tissue and show homology to known pTKs. A full-length sequence for bpTK7 (R85936) was also obtd. bpTK7 can be used to design drugs that modulate pTK activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       obtd. by
Sequence
                                                              16-APR-1996 (first entry)
EPH-like receptor protein tyrosine kinase HEK8.
EPH-like receptor protein tyrosine kinase; PTK;
human eph-like kinase; therapy; diagnosis; vect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-1994; US-222616.
(GETH ) GENENTECH INC.
Bennett BD, Goeddel D,
                                                                                                                    R85091 standard; Protein; R85091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9527061-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
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                                                                                                                                                                                                                                                                                                                                                                                                                             LLSC--SVLDSFGELIPOPSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95-366160/47.
                                                                                                                                                                                                                                                  GACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSCVNNSEEKDVPKMYCG
                                                                                                                                                                                                                                                                GACVALVSVRVYFKKCPFTVKNLAMFDDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCS
                                                                                                                                                                                                                                                                                                                     SDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDV
                                                                                                                                                                                                                                                                                                                                                            TYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPGVMGTCKETFNLYYYE
                                                                                                                                                                                                                                                                                                                                                                                                               LFSCLFGICDAVTGSRVYPANEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIR
                                                                                                                                                                                                                           TEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                       SDNDKERFIRENQFVKIDTIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFQDV
                                                                                                                                                                                                  ADGEWLVPIGNCLCNAGHEERSGECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183;
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 U04681.
US-229509
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548. .57
/label=
571. .98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 995; DB
Pred. No. 3.3e
37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
.3e-94;
                                                              PTK; HEK8; vector; ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                               antibody.
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Best Local S
Matches 183
(KROM/) KROMER L F.
(SCHU/) SCHULZ N T.
(WOUD/) WOUDE G F V.
(ZHOU/) ZHOU R.
KZOMET LF, SCHULZ NT,
WPI, 98-541751/46.
N-PSDB; V58192.
                                                                         Wus sp.

US5814479-A.

US5814479-A.

29-SEP-1998.

11-JUN-1996; 673789.

04-JAN-1994; US-177812.

11-JUN-1996; US-673789.
                                                                                                                                    4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (702946-49) from a human foetal braccDNA library. :HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced be expression of encoding sequences in procaryotic or eucaryotic host cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HEK receptors, or therespentically to modulate the activation of cell-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., us diagnostically and therapeutically to modulate receptor activa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Claim 18; Page 62-65; 133pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors.
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98-541751/46.
DB; V58192.
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                      Woude GFV,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 995; DB 1;
Pred. No. 3.3e-94;
7; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                      274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to modulate receptor activation
                                                                                                                                                                                   brain; diagnosis; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 986
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n foetal brain
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<u>ب</u>

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The present sequence represents mouse Bsk, which is a receptor-like CC The present sequence represents mouse Bsk, which is a receptor-like CC tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in CC Bsk nucleic acid probes, which can be used in detecting alterations in CC the level of Bsk messenger-RNA (mRNA) in biological samples isolated CC from a mammal afflicted with a disease, such as neurodegenerative CC diseases or disorders and neoplasms. The nucleic acid sequence can also be delivered into the limbic system of patients with limbic system CC neurodegenerative disease, disorder or injury to promote or enhance CC limbic system neuron regeneration or growth. Such neurodegenerative diseases include, chromosomal abnormalities, degenerative growth and CC development disorders, viral infections, bacterial infections, brain CC schizophrenia, or stroke and cerebral ischaemia.
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Best Loc
Matches
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01-DEC-1998.
06-JUN-1995; US-469537.
17-MAR-1995; US-406247.
17-MAR-1995; US-736559.
26-JUL-1991; US-736559.
28-CCT-1993; US-144992.
06-JUN-1995; US-469537.
(REGE-) RECENERON PHARM INC.
Maisonpierre PC, Masiakowski P, Yancopoulos GD
WPI; 99-044584/04.
                                                                                                                                                                                                                                                                                                                                                                             W83147
W83147;
Example; Fig 22; 194pp; English.

The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding prot Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor
                                                                                                                                                                                                                                                                                      Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection; neurotrophin activity; trkB; proto-oncogene; tyrosine kinase recbinding protein; BDNF; NT-3; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid probes,
messenger-RNA in bio
                                                                  proteins
                                                                                DNA encoding
                                                                                                  N-PSDB; V70207
                                                                                                                                                                                                                                                                              Rattus sp
                                                                                                                                                                                                                                                                                                                                        Rat receptor tyrosine kinase Ehk-1
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EWLVPIGKCMCKAGYEEKNGTCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGAC
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eacid prob
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                                                                                 receptor tyrosine
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bes, used in detecting alterations in level o
biological samples isolated from mammal affl
                                                                                                                                                                                                                                                                                                                                                                                         Protein; 1005
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66.2%;
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Pred. No. 9e-94;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
                                                                                 kinase
                                                                                proteins -
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afflicted
                proteins:
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Best Local
                                        treatment and diagnosis of neuronal disorders and angiogenesis related conditions.

Example 1: Page 50-53; 75pp: English.

Rat REK7 (R97853) is an eph-related tyrosine kinase receptor, for which AL-1 (see also W97854) is a ligand. Its amino acid sequence was deduced from a cDNA clone (R18893) isolated from a hippocampal cDNA library. An REK-TgG fusion was used to screen cultured cell lines for surface expression of REK7-binding activity. Primers (see also T44382-83) based on peptide sequences (R97856-59) of isolated ligands were used to amplify human breast carcinoma BTCO cell cDNA, and an amplified fragment was used to screen a human foetal brain cDNA library, leading to the isolation of AL-1 cDNA related:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-1995; U14016.
27-OCT-1994; US-330128.
07-JUN-1995; US-486449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-1997 (first entry)
Rat REK7 eph-related tyrosine kinase receptor.
REK7; eph-related tyrosine kinase receptor; AL-1; ligand;
neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH
Caras IW, Winslow
WPI; 96-239448/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine kinases. The present sequence represents rat Ehk-1. Sequence 1005 AA;
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58. .462
/label= Extracellul
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Pred. No. 1.8e
44; Mismatches
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Query Match Best Local Similarity

66

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                                                                                                                                                                                                                                                                                                                                                              4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were identified following cisolation of their encoding cDNAs (T02946-49) from a human foetal brain CDNA library. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced by expression of encoding sequences in procaryotic or eucaryotic host cells, and are used to produce antibodies (utilised in diagnostic cels, or to identify and purify ligands for HEK receptors, or therapeutically to modulate the activation of cell-associated proliferation and/or differentiation of brain cells.
                                                                                                                                                                                                             Query Match
Best Local S
Matches 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or prodn.
Claim 18; Page 54-57; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
Fox GM, Jing S, Welcher
WPI; 95-373799/48.
N-PSDB; T02947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPH-like receptor protein tyrosine kinase HEK7. EPH-like receptor protein tyrosine kinase; PTK; human eph-like kinase; therapy; diagnosis; vect
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15-APR-1994; US-229509.
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173; Conservative
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                                                                                                                                                                                                       Score 984; DB 1;
Pred. No. 4.5e-93;
4; Mismatches 42
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or prodn.

Claim 18; Page 71-75; 133pp; English.

CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,

CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,

CC 4 Novel human EPH-like receptors protein tyrosine kinases, HEK7,

CC HEK8 and HEK11 (R85089-92), respectively, were identified following

CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain

CC CDNA library. HEK5, HEK7 and HEK8 show extensive homology to the

CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8.

CC HEK1 shows no homology to any known EPH-like receptor. Recombinant

CC HEK receptors (or their soluble extracellular domains) are produced by

CC expression of encoding sequences in procaryotic or encaryotic host

CC cells, and are used to produce antibodies (utilised in diagnostic

CC assays), or to identify and purify ligands for HEK receptors, or

CC therapeutically to modulate the activation of cell-associated
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Best Local S
Matches 171
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Sequence
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EPH-like receptor protein tyrosine kinase; PTK; HEK11;
human eph-like kinase; therapy; diagnosis; antibody; vector.
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Fox GM, Jing S, Welcher
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26-OCT-1995.
14-APR-1995; U04681.
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                                   I I ENLA I F P DT VTG SEFSSL V E V R GT C V SSA E E E A E NA P R M H C SA E G E W L V P I G K C I C K A
                                                                 TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKE--
                                                                                                   TIAADESFTQGDLGERKMKLNTEVREIGPLSKKGFYLAFQDVGACIALVSVKVYYKKCWS
                                                                                                                                                                                       NWVPRNSAQKIYVELKFTLKDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID 144
                                                                                                                                                                                                                                         QAAKEVLLLDSKAQQTELEWISSPPNGWEEISGLDENYTPIRTYQVCQVMEPNQNNWLRT 87
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                                                                                                                                                                     NWISKGNAQRIFVELKFTLRDCNSLPGVLGTCKETFNLYYYETDYDTGRNIRENLYVKID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein;
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Pred. No. 3.2e
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                                                                 EDPPRMYCSTEGEWLVPIGKCSCNA
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03-JAN-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES FOR (SUGE-) SUGEN INC.
C10958c T, Millauer B,
WPI; 96-333988/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; page 109-111; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting identified 2 truncated versions, MDK1 T1 (W03422) and MDK1 T2 (W03423), of the novel mouse developmental kinase 1 (MDK1) (see al W03423), of the movel mouse developmental kinase 1 (MDK1) (see al kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential agents useful for treatment of diseases characterised by abnormal signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mouse development kinase 1 gene - used 1 diagnosis and treatment of abnormalities in
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Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase;
RTK; signal transduction; probe; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W03422 standard; Protein; W03422;
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                    TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKE--EDPPRMYCSTEGEWLVPIGKCSCNA
                                                                                                                    TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF
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IVENLAVFPDTVTGSEFSSLVEVRGTCVSSAEEEAENSPRMHCSAEGEWLVPIGKCICKA
                                                                                          TIAADESFTQGDLGERKMKLNTEVREIGPLSKKGFYLAFQDVGACIALVSVKVYYKKCWT
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600. .61
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343. .345
/label= N-glycosylation_site
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64...66
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Pred. No. 1.9e
37; Mismatches
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03-JAN-1995; UO-368776.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES FC
(SUGE-) SUGEN INC.
Clossek T, Millauer B,
                                                                                                                                                                                                                                                                                          Example 1; Page 113-115; 128pp; English.

Example 1; Page 113-115; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting identified 2 truncated versions, MDK1 T1 (W03422) and MDK1 T2 (W03423), of the novel mouse developmental kinase 1 (MDK1) (see als W03421), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse developmental kinase 1 MDK1 T2.

Mouse developmental kinase 1; MDK1 T2.

RTK; signal transduction; probe; diagnosis; gene therapy;

neurodegeneration; neuroproliferation; cancer.
                                                                                                                                                                                                                                                                          agents useful for treatment of diseases characterised by abnormal signal transduction.
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N-PSDB; T32962.
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                                                                                                                                                                                               Local Similarity 68.8 hes 172; Conservative
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                                                  TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF 204
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                                     TIAADESFTQGDLGERKKLNTEVREIGPLSKKGFYLAFQDVGACIALVSVKVYYKKCWT
                                                                                        NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID 144
                                                                                                                                           QAAKEVLLLDSKAQQTELEWISSPPSGWEEISGLDENYTPIRTYQVCQVMEPNQNNWLRT 87
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555. .57
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343. .34
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64..66
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  "product of
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                                                                                                                                                                                            Score 926.5;
Pred. No. 2e-8
37; Mismatches
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Best Local Sim
Matches 172;
                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 105-108; 128pp; English.

Mouse developmental kinase 1 (MDKI) (W03421) is a new member of eck/eph family of receptor tyrosine kinases (RTKs). Its amino acid sequence was deduced from a cDNA clone (T32960) isolated from mouse embryo and adult brain libraries. The distinct patterns of MDK1 expression during mouse development suggest an important role for MDK1 in the formation of neuronal structures. It can be used in methods for the diagnosis of diseases characterised by abnormality in a signal transduction pathway, such as neuroproliferative or neurodegenerative disorders or cancer, to screen for (ant)agonists, and to raise antibodies.
                                                                                                                                                                                                                                                                                                                                                   to screen
Sequence
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(SUGE-) SUGEN INC.
Clossek T, Millauer B,
WPI; 96-333988/33.
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03-JAN-1996; U00419.
03-JAN-1995; US-368776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse developmental kinase 1; MDK1; receptor tyrosine Mouse developmental kinase 1; MDK1; receptor tyrosine signal transduction; probe; diagnosis; therapy; neurodegeneration; neuroproliferation; cancer.
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 TVKNLAMEPDTVP-MDSQSLVEVRGSCVNNSKE--EDPPRMYCSTEGEWLVPIGKCSCNA
                                                                       TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF
                                                                                                                                        NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID
                                                                                                                                                                                      QAAKEVILLDSKAQQTELEWISSPPSGWEEISGLDENYTPIRTYQVCQVMEPNQNNWLRT
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                                                     TIAADESFTQGDLGERKMKLNTEVREIGPLSKKGFYLAFQDVGACIALVSVKVYYKKCWT
                                                                                                                     NWISKGNAORIFVELKFTLRDCNSLPGVLGTCKETFNLYYYETDYDTGRNIRENLYVKID
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and treatment of abnormalities
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Pred. No. 4e-87;
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Pasquale EB,
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Query Match
Best Local Sim
Matches 139;
Cek5+; Eph; protein tyros
prognosis.
Gallus sp.
W09515375-A.
08-JUN-1995.
07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN 1995.

08-JUN 1995.

07-SEP-1994; U10140.

03-DEC-1993; US-162809.

03-DEC-1993; US-162809.

(LJOL-) LA JOLLA CANCER R.
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Gallus sp.
WO9515375-A.
                                                                                                        Eph-related PTK Cek5+; Eph; prot
                                                                                                                                                  R75709 standard;
R75709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure: Page 92-96; 129pp; English.

Probes derived from the EPH-related Pricks Cek4 (090659) and Cek5 (090660) were used to isolate novel cDNA clones (090652-58, 090661-62) from chicken embryo and embryonic brain libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasquale EB, Sajj
WPI; 95-215256/28.
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995 AA;
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55.4%;
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Pred. No. 3.8e
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1.8e-71;
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                                                                                                                                                                                                                                                                                                                                                                WPI; 95-215256/28.

N-SSDB; Q90657.

Eph-related protein tyrosine kinase(s) - for monitoring and diagn cancer.

Claim 11; Page 71-75; 129pp; English.

Claim 11; Page 71-75; 129pp; English.

A cDNA clone encoding a novel variant of EPH-related PTK Cek5,

Cek5+ (Q90657), was isolated from a chick embryo library in lambda gtll. Cek5+ protein (R75709) contains a 16-amino acid insertion in the juxtamembrane domain, and be a result of alternative splicing. Cek5+ is exclusively expressed in the CNS. Sequence 1011 AA;
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                                                          YESVENGTVCR 278
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Title:
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O91736 xenopus lae
O07494 gailus gall
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ALIGNMENTS

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Op1694

ID 091694

Op1694

AC 091694;

PRELIMINARY;

PRT; 985 AA.

AC 091694;

PT 01-NOV-1996 (Tremblitel. 01, Created)

DT 01-NOV-1996 (Tremblitel. 12, Last annotation update)

DT 01-NOV-1996 (Tremblitel. 01, Last sequence update)

DE 0780LINE; AND LAST Sequence update;

CO Xenopus laevis (African clawed frog).

RT 11

RP SEQUENCE FROM N.A.

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PFAM; PF000069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
SEQUENCE FROM N.A.

MEDLINE; 96125143.

XU Q., ALLDUS G., HOLDER N., WILK
"Expression of truncated Sek-1 re
"egmental restriction of gene exp
hindbrain.";
Development 121:4005-4016(1995).
-:- FUNCTION: RECEPTOR FOR MEMBER
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                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Batrachia; Anura; Mesobatrachia; Pipoidea;
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(TIEMBLrel. 12, Last annotation update)
DTEIN KINASE RECEPTOR SEK-1 PRECURSOR (EC
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042422;
01-JAN-1998
01-JAN-1998
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Query Match
Best Local S
Matches 159
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EMBL, X91191; CAA62601.1; -.

HSSP, P00523; 2PTK.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PFAM; PF00041; fn3; 2.

PFAM; PF01404; EPH_Lbd; 1.

PFAM; PF01404; EPH_Lbd; 1.

PRAM; PF01404; EPH_Lbd; 1.

PRAM; PF01404; EPH_Lbd; 1.
                                                                                                                                                                                                                                                                                                                                       Transferase;
Receptor; Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PROOO14; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: EXPRESSION OCCURS IN R3, R5 AN AT LOWER LEVELS IN R2. AT LOWER LEVELS IN R2. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DC SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY). REQUIRED FOR INTERACTIONS IDENTITY OR MOVEMENT OF CELLS.
CATALYTIC ACTIVITY: AIP + A PROTEIN TYPE TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE F
                                                                                        VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                              GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                                                  VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                      WEEVSIMDEKNTPIRTYQVCNVMESSQNNWLRTDWIPRSGAQRVYVEIKFTLRDCNSLPG
                                                                                                                                                                                                                                    WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                               VDNSEEKDVPKMYCGADGEWLVPIGNCLCNAGFEEHNGGCQ
                                                                                                                  GPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRNLAQFPDTITGSDTSSLVEVRGSC
                                                                                                                                                                    VMGTCKETFNLYYYESNNDKERFIRETQYVKIDTIAADESFTQVDIGDRIMKLNTEVRDV
                                                                                                                                                                                                                                                                          Similarity 71.9
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         se; Tyrosine-protein
Transmembrane; Glyco
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      1 domain.
1 15
1 1986
6 547
6 547
3 569
1 115
325
435
533
881
108
108
1745
7745
778
3407
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                                                                                                                                                                                                                                                                                      74.58;
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3.
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TYROSINE-PROTEIN KINASE REV
EXTRACELLULAR (POTENTIAL).
POTENTIAL
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN (BY
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                        Score 894.5;
Pred. No. 1.9e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (AUTO-)
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIBRONECTIN FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase;
 PRT;
                                                                                                                                                                                                                                                                                                                                          028DBBDA CRC32;
 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding; Phosphorylation;
; Signal; Repeat;
                                                                                                                                                                                                                                                                  1.9e-79;
28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE-III
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S IN R3,
                                                                                         220
                                                               274
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                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAINS.
THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND
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SIMILARITY)
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                                                                                                                                                                                                                                                                                                    986;
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(TrEMBLrel.

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sequence update)

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Query Match
Best Local Similarity
Matches 155; Conser
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DISULFID
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
SEQUENCE
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DOMAIN
DOMAIN
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DOMAIN
DOMAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Phasianidae; Phasianinae; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y14271; CAA74643.1;
HSSP; P00523; 2PTK
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARAUJO M., NIETO M.A.;
"The expression of chick EphA7 during segmentatio peripheral nervous system.";
Mech. Dev. 68:173-177(1997).
-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNĀL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0109; TYRKINASE. PRINTS; PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATAI DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. TYPE DOMAIN.
-i- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
EPH-LIKE RECEPTOR TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEPHA7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 98092111.
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        61
                                          55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS RESTRICTED TO PROSOMERES I AND 2 IN THE DIENCEPHALON AND ALL THE RHOMBOMERES IN THE HINDBRAIN DURING SEGMENTATION STAGES. LATER ON, A SUPERLINGSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION OF SEVERAL AXONAL TRACTS. IN THE SOMITIC MESODERM, THE EXPRESSION CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST AND MOTOR AXONS THROUGH THE SCLEROTOMES.
                                    WEEISGLDENTTPIRTYQVCQVMESNQNNWLRTNWIAKSNAQRIFVELKFTLRDCNSLPG
                                                           WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycoprotein; Signal; Immunogic
1 30 POTENTIAL.
31 993 EPH-LIKE RECEPTOR TYROSINE
31 551 EXTRACELLULAR (POTENTIAL).
                                                                                                                      Conservative
                                                                                                                                                                                                                      Ä
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551
551
572
993
116
328
889
536
642
109
109
343
                                                                                                                                  71.98;
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                                                                                                                    39;
                                                                                                                  Score 862.5;
Pred. No. 2.6e
39; Mismatches
                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
-~ TEE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                           FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE C2-TYPE CYS-RICH.
                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                    6B6BFD17 CRC32;
                                                                                                                  5; DB 13;
2.6e-76;
nes 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin
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ХВ)
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                                                                                                                    Indels
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                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SIMILARITY).
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                                                                                                                Gaps
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PRELIMINARY;

PRT;

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Best Local Similarity
Matches 149; Conser
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073879;
01-AUG-1998
01-AUG-1998
01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÉPH-LIKE RELEFIC...
RTK4.
BTACHydanio rerio (Zebrafish) (Zebra danıu),
Brachydanio rerio (Zebrafish) (Zebra danıu),
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Fukaryota; Metazoa; Chordata; Craniata; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                   PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TIEMBLIEL. 07, Created)
01-AUG-1998 (TIEMBLIEL. 07, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
EPH-LIKE RECEPTOR TYROSINE KINASE RTK4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                         PFAM;
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. COOKE J.E., XU Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. COOKE J.E.;
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                181
                                                                                      182
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Genes Evol. 206:515-53
; AJ005030; CAA06303.1;
                                                                                                                                                                                                            EISGVDEHYTPIRTYQVCNYMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNNSKE--EDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
|::::| |: |:|| ||||||||| | ||||:::| |:
VSSAEEEAENSPKMHCSAEGEWLVPIGKCICKAGYQQKGDTCE
                                                                                     NSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                      SRAGEYLAFQDVGACIALVSVHVFYKKCPLAVRNLAQEPDTVTGADTSSLVEVRGSCVD
                                                                                                                      VNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVN
                                                                                                                                                                 GTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGP 122
                                                                                                                                                                                              GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSEEQEVPKMYCGADGEWLVPIGNCLCNPGYEERNEQCQ
                                                                                                                                                     GTCKETFNLYYLESDSDNERYAHESRFSKIDTVAADESFTQVDIGDRIMKLNTEVRDVGV
                                                                                                                                                                                                                                                                                                                                  PF01404;
PF00069;
PF00041;
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                                                                                                                                                                                                                                                                                                                                                                                                               2DB-GENE-990415-61; rtk4
                                                                                                                                                                                                                                                                                                                                                                                                                          P00523; 2PTK.
                                                                                                                                                                                                                                                                                                880
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                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 pkinase;
fn3; 2.
                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                             880
                                                                                                                                                                                                                                                                                                  98862 MW;
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                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                           Score 838.5; DB Pred. No. 5e-74; 6; Mismatches
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                                                                                                                                                                                                                                                                                                  7C139606 CRC32;
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tariophysi; Cypriniformes;
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                                                                                                                                                                                                                                                                 DB 13;
                                                                219
                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277
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                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                  1 880;
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                                                                                                                                                                                                                                           Gaps
                                                                                                                              181
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OF THE THE TREET TO THE TREET AND ADDRESS AND ADDRESS TO THE TREET THE TREET
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                                                            Query Match
Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZFIN; ZDB-GENE-990415-58; Zek1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR, 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FF
PFAM; PF00069; Pkinase; 1.

PFAM; PF00036; SAM; 1.

PFAM; PF00036; SAM; 1.

PFAM; PF00041; fn3; 2.

PRINTS; PR00104; TYRKINASE.

PRINTS; PR00014; FNYYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
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VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
HSSP;
ZFIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygil; Teleostei; Buteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
EPH-LIKE KINASE 1 PRECURSOR (EC 2.7.1.1112) (TYROSINE-PROTEIN KINASE
RECEPTOR ZEK1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Novel Eph-family receptor tyrosine kinase developing zebrafish nervous system."; Dev. Dyn. 209:166-181(1997).
-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 97329578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOVENKAMP D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZEK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Tyrosine-protein kinase; ATP-binding;
                        ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TYPE TISSUE SPECIFICITY: WIDELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM.

CAPALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROLE IN EARLY PATTERN FORMATION
WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U89295; AAC60220.1;
P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GREER P.;
                                                                              63.0%;
                                                                                                                                                                  109654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Sig
BY SIMILARITY
EPH-LIKE KINF
                                                            ; Score 755.5; DB
; Pred. No. 8e-66;
37; Mismatches 4
                                                                                                                                                                  ₹
                                                                                                                                                                        ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
S -> N.
                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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                                                                                                                                                             -> N.
10D38182
                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal;
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FALSE_NEG.
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IN THE DEVELOPING ZEBRAFISH
                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IN-B FAMILY.
DEVELOPING
                                                            Indels
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                                                                                                   Length
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                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
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                                                                                                   981;
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PFAM; PF001404; EPH_lbd; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF000536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           043477;
01-JUN-1998
01-JUN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE; 96134673.

IKEGAKI N., TANG X.X., LIU X.G., BIEGEL J.A.,

SULMAN E.P., BRODEUR G.M., PLEASURE D.E.;

"Molecular characterization and chromosomal lo

(EPHT3): a developmentally regulated human pro

gene of the EPH family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TANG X.X., PLEASURE D.E., Submitted (SEP-1997) to t EMBL; AF025304; AAB94602.
                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0014; FNTYPEIII.
PRINTS; PRO0109; TYRKINASE.
Tyrosine-protein kinase.
SEQUENCE 1055 AA; 117492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      043477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172
                                                                                                                                    103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                             61
                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                            Local Similarity
mes 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
                                                                                                                                                                                                                                               1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol.
                                                                                                                               TCVEDAEELEGPRMFCSADGGWLVPIGRCVCRPGFEEVDGHCQ
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                                                               IREVGPVNKKGEYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEV
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                                             VRSFGPVSRSGFYLAFQDYGGCMSLIAVRVFYRKCPRIIQNGAIFQETLSGAESTSLVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P00523;
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(TrEMBLrel.)
(OSINE KINASE)
                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                     559
                                                                                                                                                                                                                                                                                                                                                                                                                       117492
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06, Las
12, Las
EPHB2V.
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                                                                                                                                                                                                                                                                                                              49;
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                                                                                                                                                                                                                                                                                                                              Score 708; DB 4; Length 1055; Pred. No. 4e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
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kinase
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                                                                                                                                                                                                                                                                                                          Gaps
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PROSITE: PS00343; GRAM_POS_N
PROSITE: PS00107; PROTEIN_KI
PROSITE: PS00109; PROTEIN_KI
PROSITE: PS00790; RECEPTOR_T
PROSITE: PS00791; RECEPTOR_T
PROSITE: PS00791; RECEPTOR_T
PROSITE: PS00791; RECEPTOR_T
PFAM; PF00069; Pkinase; 1.
PFAM; PF00059; Pkinase; 1.
PFAM; PF01404; EPH_lbd; 1.
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Q91571;
                                           NP_BIND
DISULFID
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID BLASTULA TRANSITION AND REAPPEARS AT LATE MEDURULATION. EXPRESSED AT HIGHER LEYELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC STAGES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBIQUITOUSLY EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OYARY. EXPRESSION ITHE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE RETINA OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALLYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-- EMBL; U14164; AAA74888.1; --
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                             TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                             Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JONES T.L., KARAVANOVA I., MAENO M., ONG R.C., KUNG H.-F., DAAR I.O.;
"Expression of an amphibian homolog of the Eph family of receptor
tyrosine kinases is developmentally regulated.";
Oncogene 10:1111-117(1995).
Oncogene 10:111117(1995).
Oncogene 10:11117(1995).
Oncogene 10:111117(1995).
Oncogene 10:111117(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TremBirel. 01, Created)
01-NOV-1996 (TremBirel. 01, Last sequence update)
01-NOV-1999 (TremBirel. 12, Last annotation update)
EPHRIN TYPE-B RECEPTOR XEK PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; U14164;
; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||: |::| | | ::||: :||||||||:| | | ||:| | | :|:
RGSCIANAEEVDVPIKLYCNGDGEWLVPIGRCMCKAGFEAVENGTVCR 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO0109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95215070.
                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ); GRAM_POS_ANCHORING; UNKNOW

; PROTEIN_KINASE_ATP; 1.

); PROTEIN_KINASE_TYR; 1.

); RECEPTOR_TYR_KIN_V_1; FALS

L; RECEPTOR_TYR_KIN_V_2; 1.
Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                           POLY-LEU
EXTRACELLULAR (POTENTIAL
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
                                                            PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
                 PHOSPHORYLATION (AUTO-) (POTENTIAL). POTENTIAL.
                                                                                                                                                                            FIBRONECTIN TYPE-III.
                                                                                                                                                                                                       FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                  EPHRIN TYPE-B
                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase; ATP-binding; Phosphorylation;
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Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TYROSINE-PROTEIN
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Matches
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                                                                                                                                                                                                                        STEIN E., SCHOECKLMANN H.O., I
SUDMITTED (DEC-1997) to the EN
EMBL; AF03733; AAB94628.1; -
EMBL; AF037334; AAB94628.1; -
HSSP; P08631; 2HCK.
PFAM; PF00041; fn3; 2.
PFAM; PF000536; SAM; 1.
PFAM; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TIEMBLIE1. 06, Created)
01-JUN-1998 (TIEMBLIE1. 06, Last sequence update)
01-NOV-1999 (TIEMBLIE1. 12, Last annotation updat
EPH-LIKE RECEPTOR TYROSINE KINASE HEPHBIC
(EPH-LIKE RECEPTOR TYROSINE KINASE HEPHBID).
                                                                                                                                                                                                                                                                                                                                                                                                                                    043569
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-KIDNEY;
                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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            176
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Local
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                          WEEISGYDEHYTPIRTYQYCNYMDHSQNNWLRTNWYPRNSAQKIYYELKFTLRDCNSIPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLGTCKETFNLYYMESDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTE 116
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RGSCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE-ERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGSCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE-ERGFMCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
125; Conserv
                                                                                                                                                al Similarity
123; Conserv
                                                                                                                                                                                                          PR00109;
PR00014;
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985 /
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                                                                                                                                                                                                                                                                                                                                                       Metazoa;
                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  (Human)
                                                                                                                                                                                               A,
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                                                                                                                                                                                                        TYRKINASE.
FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                              Chordata; Cr
                                                                                                                                                                                               105291 MW;
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                                                                                                                                                         56.4%;
54.2%;
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55.1%;
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Pred. No. 1.5e
47; Mismatches
                                                                                                                                              Score 676.5; DB 4;
Pred. No. 4.3e-58;
5; Mismatches 52;
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                                                                                                                                                                                                                                                                                                        DANIEL
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1; 2416A8F9 CRC32;
                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                        T.O.;
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                                                                                                                                                                 Length
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222

RGTCIPNAEEVDVPIKLYCNGDGEWMVPIGRCTCKPGYEPENSVACK 268

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Best Local Similarity 54.3
Matches 123; Conservative
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095143;
01-MAY-1999
01-MAY-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-KIDNEY;
TISSUE-KIDNEY;
STEIN E., SCHOEKLMANN H.O.,
Submitted (NOV-1997) to the !
EMBL; AF037332; AAD02031.1;
HSSE; P00523; 2PTK.
          PROSITE;
                         "Nck recruitment to Eph recuto c-Jun Kinase.";
J. Biol. Chem. 0:0-0(1997).
EMBL; AF037331; AAD02030.1;
HSSP; P00523; 2PTK.
                                                                                                                                                                 095142
                                                                 TISSUE-KIDNEY;
STEIN E., HUYNH-DO U.,
                                                                                                                                01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-NOV-1999 (TrEMBLrel. 12,
EPH-LIKE RECEPTOR TYROSINE K
                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
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  Receptor;
                                                                                                                           EPHB1.
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                                                                                                   Sutheria;
                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                   211
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                                                                                                                                                                                                                                                VRSFGPLTRNGFYLAFQDYGACMILLSVRVFFKKCPSIVQNFAVFPETMTGAESTSLVIA
                                                                                                                                                                                                                                                         IREVGPVNKKGEYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEV
                                                                                                                                                                                                                RGTCIPNAEEVDVPIKLYCNGDGEWMVPIGRCTCKPGYEPENSVACK
      0523; 2PTK.
PS00107; PROTEIN_KINASE_ATP;
PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                        Kinase.
973 AA
                                                                                                 Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa;
                                                                                                         Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                          PRELIMINARY;
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ABLrel. 10,
ABLrel. 12,
TYROSINE F
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                                                                                                Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
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                                                        LANE A., CE
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                                                                                                                                 , Last sequence update)
, Last annotation updat
KINASE HEPHB1.
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                                                                                                                                                        Created)
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EMBL/GenBank/DDBJ
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Pred.
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                                                        CERRETTI D.P
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Mismatches
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No. 4.5e-58;
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                                                                .P.,
                                                                                                                                        update)
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                                                                                                                                                                                                                                                                                                                                                52;
                                                         couples
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                                                                DANIEL
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                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                         Mammalia;
                                                        L T.O.;
ligand
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                                                         activation
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Best Local S
Matches 123
                                              EMBL; L43620; AAA93526.1; ...

HSSP; P00523; 2PTK.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PRAM; PF00041; fn3; 2.

PFAM; PF00040; fn3; 2.

PFAM; PF000536; SAM; 1.

PFAM; PF01404; EPH_Lbd; 1.

PFAM; PF01404; EPH_Lbd; 1.

PFAM; PF01404; EPH_Lbd; 1.

PFAM; PR00109; TYRKINASE.

PRINTS; PR00010; TYRKINASE.

PRINTS; PR000104; FNTYPEIII.
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Q91735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 96068901.
SCALES J.B., WINNING R.S., RENAUD (
"Novel members of the eph receptor during Xenopus development.";
Oncogene 11:1745-1752(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLIE). 01, Created)
01-NOV-1996 (TIEMBLIE). 01, Last sequence update)
01-NOV-1999 (TIEMBLIE). 12, Last annotation update)
EPHRIN TYPE-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996
                    Transferase; Tyrosine-protein kinase;
Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASE RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE IN THE EMBRYO IN PRE-SOMITIC MESODERM, CAUDAL SOMITIES, MIDBRAIN, AND CEMENT GLAND. MOST ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER LEVE IN INTESTINE, KIDNEY, OVIDUCT AND PHARYIN.

DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 1 INMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPGSCKETFNLYXYETDSVIATKKSAFWSEAPYLKVDTIAADESFSQVDFRGRLMKVNTE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IREVGPVNKKGFYLAFQDVGACVALVSVRYIFKKCPFTVKNLAMFPDTVP-MDSQSLVEV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLGTCKETFNLYYMESDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>8</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110041 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOR MEMBERS
Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RENAUD C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 676.5; 1
Pred. No. 4.6e
45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DF5C8ED3 CRC32;
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                                ATP-binding; Phosphorylation;
                  Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , DB 4,
4.6e-58;
52;
                                                                                                                                                                             SHEA L.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHRIN-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinase
                Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SARGENT T.D.; subfamily expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220
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                                                                                                                                                                                                                                                                                                                                                                                                                  LEVELS
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RESULT
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                                   Oncogene 8:1807-1813(12).

EMBL; Z19661; CAA79511.1; -.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PFAM; PF001404; EPH_1bd; 1.

DR PFAM; PF00041; fn3; 2.

DR PFAM; PF00536; SAM; 1.

DR PFAM; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.:
Best Local Similarity 53.:
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Q07498;
Q07498;
Q1-NOV-1996
Q1-NOV-1996
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DISULFID
BINDING
ACT_SITE
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CARBOHYD
CARBOHYD
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phasi
                                                                                                                                                                                                                               expressed.";
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=EMBRYO;
               Transferase.
NON_TER
                                                                                                                                                                                                                                             "Five novel avian Eph-related
                                                                                                                                                                                                                                                                 SAJJADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217
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1996 (TremBLrel. 01, 1
1999 (TremBLrel. 12, 1
E KINASE CEK10 RECEPTO
                                                                                                                                                                                                                                                            F.G., PASQUALE
                                                                                                                                                                                               8:1807-1813(1993).
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886
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AA.
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el. 01, Last sequ
el. 12, Last anno
0 RECEPTOR (EC 2.
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                                                                                                                                                                                                                                                                                                                                            Phasianidae;
MW;
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ATP (BY
BY SIMIL
ATP (BY
BY SIMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE DOMAIN. CYS-RICH.
                                                                                                                                                                                                                                                                                                                                    Craniata; Vertepraca,
Annidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPHRIN TYPE-B RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                             tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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C5CA9B7B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BD419F6D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
annotation update)
EC 2.7.1.112) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
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(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              988
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                                                                                                                                                                                                                                                                                                                                                            Vertebrata;
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.5e-57;
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                                                                                                                                                                                                                                                                                                                                                            Archosauria;
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Best Local S
Matches 117
                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q60669;
Q60669;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHB3 OR ETK2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                   PFAM;
PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U11493; AAA67925.1;
HSSP; P00523; 2PTK.
MGD; MGI:104770; Ephb3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12, PROTEIN KINASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 95200798.
 117
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                                     119
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                                                                                                                                                                                                                                                                                                                                            4; PF01404; EPH_1bd; 1.

4; PF00041; fn3; 2.

4; PF00536; SAM; 1.

4; PF00069; Pkinase; 1.
                                                                                                                                          WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
SFGPLSKAGFYLGFQDQGACMSLISVRAFYKKCASTTAGFALFPETLTGAEATSLVIAPR
                    EVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRG
                                                                  GTCKETFNLYYMESDDD----HGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIR | :|||||||| | ::||::|| ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|::|::|::|::|::|::|::|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::||::|::|::|::|::|::|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGTCIPNAVEVSVPLKLYCNGDGEWMVPVGACTCAAGYEPAMKDTQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLGTCKETFNLYYMESDDD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGSCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYEE--RGFMCQ
                                                                                                                                                                                                                      108;
                                                                                                                                                                                                                  Similarity 49.8
08; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 51.3
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  ::104770; Ephb3:
PS00790; RECEPTOR_TYR_KIN_V_1;
PS00791; RECEPTOR_TYR_KIN_Y_2;
PS00107; PROTEIN_KINASE_ATP; 1
PS00109; PROTEIN_KINASE_TYR; 1
                                                                                                                                                                                                                                                                                                             938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                             103996
                                                                                                                                                                                                                                   49.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.7%;
51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROBERTSON
                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -HGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTE
                                                                                                                                                                                                                Score 589; DB 11;
Pred. No. 1.7e-49;
5; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 644; DB 13;
Pred. No. 7.1e-55;
18; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                             2B01D2A0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinases
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Г.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myocardium
                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVNTK
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                  177
                                                                                                                                              60
                                                                                                                                                                              62
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  Query Match
Best Local Similarity
Matches 102; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PRAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN THE BRAIN AND SPINAL CORD AND IN THE FIRST AND FOURTH VISCERAL ARCHES. MOST ABUNDANT IN ADULT BRAIN, WITH LOWER LEVELS IN EYE, HEART, OVARY OVIDICT, LUNG AND PHARYNX.

-!- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-- BIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                        NP_BIND
DISULFID
BINDING
ACT_RISE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   091736;
01.NOV-1996 (TIEMBLrel. 01, Created)
01.NOV-1996 (TIEMBLrel. 01, Last sequence update)
01.NOV-1999 (TIEMBLrel. 12, Last annotation update)
EPH RECEPTOR TYROSINE KINASE (XELK) (FRAGMENT).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE; 96068901.

SCALENE; 96068901.

SCALES J.B., WINNING R.S., RENAUD C.S., SHEA

"Novel members of the eph receptor tyrosine
during Xenopus development.";

Oncogene 11:1745-1752(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase;
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                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE 213 :|: |: | ::||::||:| |:| |:| ACIANAVEVSVPLKLYCNGDGEWMVPVGACTCATGHE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                  460
481
<101
101
238
348
348
          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tyrosine-protein kinase;
                                                                                                                                                                             100850
                         47.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE
  score 563.5; DB 13;
pred. No. 5e-47;
42; Mismatches 34;
                                                                                                                             ¥.
                                                                                                                                                                                                                                         PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
ENGREEMENTY.
                                                                                                                        POTENTIAL.
POTENTIAL.
W; C096D006
                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE DOMAIN (
                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                          FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR
                                                                                                                                                                                                                       PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Phosphorylation;
; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHEA L.J.,
sine kinase
                                                                                                                        CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SARGENT T.D.;
subfamily expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            AB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amphibia;
                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
                                                  902;
  7;
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Gaps
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                                                                                                                                                                   Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q07494
Q07494;
01-NOV-1996 (TIEMBLrel. 01, C.
01-NOV-1996 (TIEMBLrel. 01, L.
01-NOV-1999 (TIEMBLrel. 12, L.
                                                                                                                                                                                                                                             PFAM; PF000536; PFAM; PF00069; PFAM; PF01404; PF01404;
                                                                                                                                                                                                                                                                                    Oncogene 8:1807-1813(1993).
EMBL; Z19110; CAA79526.1; -.
HSSP; P00523; 2PTK
PROSITE; PS00107; PROTEIN_KI;
PROSITE; PS00109; PROTEIN_KI;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phasi
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                          expressed
                                                                                                                                                                                                                                                                                                                                                    SAJJADI F.G., PASO
"Five novel avian
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
 171
                      176
                                           139
                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 HVVCK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159
                                                                                    83
                                                                                                       61
                                                                                                                            23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                              VLGTCKETFNLYYMESDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTE
                                                                                                                                                WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVK----FREHQFTKIDTIAAD
                                                                                                                           WEEVSGYDENLNTIRTYQVCNVFEPNQNNWLLTTFINRRGAHRIYTEMRFTVRDCSSLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVFPETMTGAESTSLVIARGTCIPNAEEVDVPIKLYCNGDGEWMVPIGKCTCKAGYEPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVYVEMRFTVRDCSSLPNVPGSCKETFNLYYYETDSNIDNKISTFWNESPYLKVDTIAAD
            RGSCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE-ERGFMCQ
                                                                                  VPGSCKETFNLYYYETDSVIATKKSAFWTEAPYLKVDTIAADESFSQVDFGGRLMK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE-ER
RGTCIPNAEEVDVPIKLYCNGDGEWMVPIGRCTCKAGYEPENNVACR
                                                            IREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEV 175
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pkinase;
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PROTEIN_KINASE_TYR;
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Eph-related
                                                                                                                                                                                                                          105994 MW;
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Last annotation update)
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Pred. No. 7.7e
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Job time: 2372 sec

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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen
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EPA4_CHICK
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062413 mus musculu
007496 gallus gall
P54764 homo sapien
003137 mus musculu
260629 mus musculu
P54757 rattus norv
P54756 homo sapien
061772 mus musculu
015375 homo sapien
P54759 rattus norv
09127 mus musculu
P54753 gallus gall
P28693 gallus gall
P28693 gallus gall
P29323 homo sapien
P54764 nus musculu
P09759 rattus norv
P54764 homo sapien
P54764 homo sapien
P54765 homo sapien
P54766 homo sapien
P54761 mus musculu
P64761 mus musculu
P64763 homo sapien
P64761 mus musculu
P64763 homo sapien
P64764 mus musculu
P64765 homo sapien
P64766 homo sapien
P64766 homo sapien
P64768 sarcophyton
P64043 homo sapien
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008680 rattus norv
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P11835 mus musculu	P53714 sus scrofa	P24870 saccharomyc	P96156 vibrio furn	P52701 homo sapien	Q9zj63 helicobacte	Q58295 methanococc	P05471 kluyveromyc	Q60675 mus musculu	P39677 saccharomyc	P54873 arabidopsis	

ALIGNMENTS

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RESOLUTION ACCOMENS OF THE PROPERTY OF THE PRO
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PFAM; PFO
                                                                                                                                                                                                                                                                                                         008680;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112)
KINASE RECEPTOR REK4).
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DOMAIN
STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 98120505.
Li Y.Y., McTlernan C.F., Feldman A.M.;
"IL-1 beta alters the expression of the r-EphA3 in neonatal rat cardiomyocytes."
                                                                                                                                                                                              Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAI
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SITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1
SITE; PS01186; EGF_2; UNKNOWN_1.
M; PF00041; fn3; 2.
M; PF00041; fn3; 2.
M; PF00069; pKinase; 1.
M; PF000569; SAM; 1.
M; PF00536; SAM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
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BY SIMILARITY.

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 5.6
0; Mismatches
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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-> L (IN CAA01906).
B8D900FA80FF5121 C
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                                                                                                                                                                                                          Vertebrata;
ae; Murinae;
                              receptor
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6.6e-103;
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                              tyrosine kinase
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Rattus.
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Best Local S
Matches 217
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00709; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF000536; SAM; 1.
PFAM; PF001404; EPH_lbd; 1.
                                                                                                                                                                                                                                                         ACT_SITE
MOD_RES
CARBOHYD
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DOMAIN
NP_BIND
BINDING
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0014; FNTYPEIII. PRINTS; PRO0109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U69278; HSSP; P16109;
                                                                                                                                                                                                                                                 SEQUENCE
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  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE
                                                                                                                                          WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                        VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
 NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                            VLGTCKETFNLYYMESDDDHGVKFLEHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                                                                                                                             WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 274:H331-H341(1998).
RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
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6. 89
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYS RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                            Score 1186; DB 1;
Pred. No. 1.1e-101;
                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
9; F170C49312F7A0AB CRC64;
                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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 220
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232 NNSKEEDPPRMYCSTEGEWLVPIGKCTCNAGYEERGFICQ 271

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RESULT 3

EPA3_MOUSE
ID EPA3_M
AC P293]M
AC P293]M
AC P293]M
AC P293]M
AC P293
O1 -NOV
DE EPHANIN
DE EPHANIN
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OC EUKARY
OC --- SI
CC -
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PRINTS; PRO0014; ENTYPEIII.

PRINTS; PRO00109; TYRKINASE_ATD; 1.

PROSITE; PS00107; PROTEIN_KINASE_TVR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TVR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROM; PF00064; fn3; 2.

PFAM; PF00065; pkinase; 1.

PFAM; PF00064; Fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992
01-DEC-1992
01-NOV-1997
                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                  Receptor;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          At least two forms of the receptor.";

New Biol. 3:769-778(1991).

-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.

-!- CAPALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE BY ADERBY E - II-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sajjadi F.G., Pasquale E.B., Subramani S.; "Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 92031278.
Sajjadi F.G., Pasquale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINASE RECEPTOR ETK1) (MEK4).
EPHA3 OR ETK1 OR MEK4 OR TYRO4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A45583; A45583.
HSSP; P16109; 1FSB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRAIN.
SIMILARITY: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M68513; AAA39521.1;
M68515; AAA39522.1;
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                                                                                                                                                                                                    Transmembrane;
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                                                                                                                                                                                           Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Alternative splicing
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                          e: Glycoprotein; Signal; Alternati
BY SIMILARITY
EPHRIN TYPE-A RECEPTOR 3.
EXTRACELLULAR (POTENTIAL).
EOTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYS-RICH.
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  FIBRONECTIN TYPE-III.
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A3_CHICK

DEPA3_CHICK

C P29318;

C P29318;

T 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 35, Last sequence update

DT 01-NOV-1997 (Rel. 35, Last annotation upda

DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.

DE KINASE RECEPTOR ETK1) (CEK4).

GN EPHA3 OR ETK1 OR CEK4

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata;

N=>qnathae; Galliformes; Phasianidae; P
                                                                                                    X MEDLINE; 92031278.

XA MEDLINE; 92031278.

XA Sajjadi F.G., Pasquale E.B., Subramani S.;

RT and Sajjadi F.G., Pasquale E.B., Subramani S.;

RT "Identification of a new eph-related receptor tyrosine kinase gene

RT from mouse and chicken that is developmentally regulated and encodes

RT at least two forms of the receptor.";

RL New Biol. 3:769-778(1991).

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO

CC EPHRIN-A2, -A3, -A4 AND -A5.

CC -1- FUNCTION: ACTIVITY ATP + A PROTEIN TYROSINE - ADP +

CC PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN TH
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between
the Eurc
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VARSPLIC
SEQUENCE
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MOD_RES
CARBOHYD
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NP_BIND
BINDING
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 92031278.
                                                                          BRAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATI-
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
            tween the Swiss Institute of Bioinf European Bioinformatics Institute.
by non-profit institute.
                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNSKEEDPPRMYCSTEGEWLVPIGKCTCNAGYEERGFICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLGTCKETFNLYYMES-DDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217;
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635
653
746
779
336
336
492
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98.6%;
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                                                                                                                                                                                                                                                                                                                         data; Craniata; Vertebrata;
Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
BEJEACH (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
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Pred. No. 8.3e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                     update
           long
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C 2.7.1.112)
            There are no rest
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3.3e-101;
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                                                                                                                                                                                                                                                                                                                                                                                           (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                          Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                       Archosauria;
                       restrictions
                                       LEMBL
                                     a collaboration - MBL outstation
                                                                                                                                                                                                                                         encodes
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Query Match
Best Local Similarity
Matches 208; Conserv
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PRINTS; PR00109; TYRKINASE.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGEPTOR_TYR_KIN_V_2; 1.
         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update
EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.
KINASE RECEPTOR EHK-2) (EPH HOMOLOGY KINASE
EPHA6 OR EHK2 OR EHK-2.
                                                                           EPA6_RAT P54758;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
NP_BIND
BINDING
                                                                                                 RAT
                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor; SIGNAL
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or send a
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DOMAIN
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PFAM;
PFAM;
PFAM;
     Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M68514; AAA48666.1; -. PIR; B45583; B45583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                            181
                                                                                                                                                                                                     121
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                                                                                                                                                                                            GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV
                                                                                                                                                                                                                                                              WEEISGVDEHYTPIRTYQESNYMDHSQNNWLRTNWIPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                          WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
                                                                                                                                      NHSKEEEPPKMYCSTEGEWLVPIGKCLCNAGYEERGFACQ
                                                                                                                                                                               GPVSKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00041; fn3; 2.
PF00069; pkinase; 1.
PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01404; EPH_1bd; 1.
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an email t
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illarity 94.5%;
Conservative
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                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   license agreement (See http://www.isb-sib.ch/announce/
license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             109910
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Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                       Score 1139; I
Pred. No. 2.4e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
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ATP (BY
ATP (BY
BY SIMIL
                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (AUTO-) (BY POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPHRIN TYPE-A RECEPTOR EXTRACELLULAR (POTENTIA
                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                           E8895F0BDF77651E CRC64;
                     ion update)
(EC 2.7.1.112) (TYROSINE-PROTEIN
GY KINASE-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                          N KINASE.
Y SIMILARITY).
Y SIMILARITY).
                                                                                    948
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2.4e-97;
hes 6;
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                                                                                                                                      270
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                                                                                                                                                                                                                                                                                                                            Length 983
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SGREDATA

Last

sequence update

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Query Match
Best Local
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PRINTS; PRO0109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
5_MOUSE
EPA6_MOUSE
Q62413;
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         malsonplerre P.C., Barrezueta N.X., Yancopoulos G.D.;
"Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression oncogene 8:3277-3288(1993).
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
NP_BIND
NP_BIND
ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: RECEPTOR FOR MEMBERS OF -1- CATALYTIC ACTIVITY: ATP + A PROTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P00523;
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                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE
                                                                                                                                                      VKSSEERDTPKLYCGADGDWLVPLGRCICTTGYEE
                                                                                                                            VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                                                                                                        VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                           WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                               il Similarity
159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
 (Rel.
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2PTK
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                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     106235
                                                                                                                                                                                                                                                                                                                        76.2%;
             Created)
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                                                                                                                                                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                                                                                                                                                                                      EPHRIN TYPE-A RECEPTOR 6.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
AIP (BY SIMILARITY).
AIP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                           Score 914.5; DB 1;
Pred. No. 1.2e-76;
Pred. No. 24;
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                             A47DC78EDB2DEF30 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
                                      ₿
                                                                                                      270
                                                                                                                              214
                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                              ۲,
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                               179
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Query Match
Best Local S
Matches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS00109; PROTEIN_KINASE_TYX; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; PROSITE; PS001791; RECEPTOR_TYR_KIN_V_2; PROSITE; PS00146; EGF_2; UNKNOWN_1.

PFAM; PF00041; fn3; 2.

PFAM; PF000536; SAM; 1.

PFAM; PF001404; EPH_1bd; 1.
                                                                                                                                                                                                              DOMAIN
NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the Exhit the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U58332; AAB53836.1; HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee A.M., Navaratnam D., Ichimiya S., Greene M.I., Davis J.G.;
"Cloning of m-ehk2 from the murine inner ear, an eph family receptyrosine kinase expressed in the developing and adult cochlea.";
DNA Cell Biol. 15:817-825(1996).

-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHRIN-A1, -A2, -A3, -A4 AND -A5
-!- CATALYTIC ACTIVITY: ATP + A PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHA6 OR EHK2 OR EHK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOY-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-2) (EPH HOMOLOGY KINASE-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0014; FNTYPEIII. PRINTS; PRO0109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 97047913
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  61
                                        56
                                                                                                                    Local Similarity
les 159; Conser
                                                                            ,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATI-
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:10803
                                                        WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                                    WDAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKFTLRDCNSIPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
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RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                                                                                      1035
549
570
1035
943
644
662
797
                                                                                                                              76.2%;
74.0%;
                                                                                                                                                                                                                116137
                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
MW; 560B264
                                                                                                                                  Score 914.5; DB 1
Pred. No. 1.3e-76;
                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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                                                                                                                  Mismatches
                                                                                                                                                                                                            560B264194A5EF74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
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                                                                                                                                                    DB 1;
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                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
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PFAM; PFAM; PFAM;

PF00041; PF00069; PF00536;

; fn3; 2. ; pkinase; ; SAM; 1.

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RESULT 7
EPA4_CHICK
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                               PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPA4_CHICK
Q07496; Q90772;
Q1-NOV-1997 (Re
                                                                                                                                           EMBL; D38174;
EMBL; Z19059;
HSSP; P00523;
                                                                                                                                                                                                                                                                This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8).
                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                        Oncogene 8:1807-1813(1993).

-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
-!- EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sajjadi F.G., Pasc
"Five novel avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE-SPINAL CORD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPHA4 OR CEK8.

Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                                                                                                           expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 96404128.
Ohta K., Nakamura M.,
Ando M., Tanaka H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The receptor tyrosine kinase, subtypes of motoneurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
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                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                             2PTK.
                                                                                                                                                      BAA07373.1;
CAA79509.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasquale
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Eph-related
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development.";
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THE CATALYTIC
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RESULT 8
EPA4_HUMAN
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Best Local S
Matches 162
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NP_BIND
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RES
CARBOHYD
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CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                   EPA4_HUMAN STANDARD; PRT; 986 AA.

EPA4764;

D1-OCT-1996 (Rel. 34, Created)

O1-OCT-1996 (Rel. 34, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.1.12) (TYROSINE-PROTEIN KINASE RECEPTOR SEK) (RECEPTOR PROTEIN-TYROSINE KINASE HEK8).

EPHA4 OR SEK OR HEK8.

HOMO Saplens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor;
                                                                        "cDNA cloning and tissue distribution protein-tyrosine kinases."; Oncogene 10:897-905(1995).
                                                                                                     Fox G.M., Holst P.L.,
Basu R., Welcher A.A.;
                                                                                                               TISSUE-BRAIN;
MEDLINE; 95206782.
Fox G.M., Holst P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                  Eutheria;
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FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

SUBJECTIOUR PHOSPHATE.
SUBJECTIOUR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CA
                                                                                                                                                                                                                                                                                                                                                                                                                                        WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
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ferase; Tyrosine-prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    il Similarity
162; Conser
                                                                                                                                                                  Primates;
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548
570
325
436
621
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73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109482
                                                                                                               Chute H.T.,
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POTENTIAL
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SOURCE (IN REF. 2).
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Pred.
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CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III (BY

FIBRONECTIN TYPE-III (BY
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ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
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(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                              Lindberg R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            910.5;
No. 2.
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SIMILARITY).
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RESULT 9
EPA4_MOUSE
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Best Local Similarity
Matches 162; Conserv
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PRINTS; PRODIO19; TYRKINASE_ATP; 1.

PROSITE; PSODIO17; PROTEIN_KINASE_ATP; 1.

PROSITE; PSODIO19; PROTEIN_KINASE_DOM; 1.

PROSITE; PSODO11; PROTEIN_KINASE_DOM; 1.

PROSITE; PSOO790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PSOO791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PSOO791; RECEPTOR_TYR_KIN_V_2; 1.

PRAM; PFOO041; fn3; 2.

PFAM; PFOO046; PKINASE; 1.

PFAM; PFOO0516; SAM; 1.

PFAM; PFOO0516; SAM; 1.

TIANSFERASE; TYTOSINE-PTOTEIN KINASE; ATP-

TIANSFERASE; TYTOSINE-PTOTEIN KINASE; ATP-
 EPA4_MOUSE
Q03137;
Q1-OCT-1994
Q1-OCT-1994
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
NP_BIND
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BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
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HSSP; P00523;
MIM; 602188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
SIGNAL
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                          VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                  VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ
                                                                                                                                                                                                                                WEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
  (Rel.
(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                A.
                                             STANDARD;
  30,
                                                                                                                                                                                                                                                                                     75.5%;
73.3%;
                                                                                                                                                                                                                                                                                                                                109859
Created)
Last sequence up
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                               MW;
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FIBRONECTIN TYPE-III (BY S
FIBRONECTIN TYPE-III (BY S
FIBRONECTIN TYPE-III (BY S
FROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                                                                        Score 905.5;
Pred. No. 8.2e
30; Mismatches
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POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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EXTRACELLULAR
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                                                                                                                                                                                                                                                                                     905.
                                             986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                                                   DB 1,
3.2e-76;
28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR 4. (POTENTIAL).
                                                                                                                     220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                986;
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                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                179
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                                                                                                                                            233
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RAMEDLINE; 93205393.

RA Gilardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,
RA Gilardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,
RA Chestier A., Wilkinson D.G., Charnay P.;
RL Oncogene 8:1103-1103(1993).

CC EPHRIN-A1, "A4 AND A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-3.
CC MAY PLAY A ROLE IN A SIGNAL TRANSDUCTION PROCESS INVOLVED IN
CC HINDBRAIN PATTERN FORMATION.
CC I-CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
CC I-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC I-SUBCELLULAR LOCATION: TYPE I SITE MAY BE GENERATED BY
CC I-SUBCELLULAR PROTEIN SPECIFIC IN THE BRAIN, LOWER LEVELS
CC IN THE HEART, LUNG AND KIDNEY. IT IS SEGMENTALLY EXPRESSED
CC IN THE EMBRYONIC BRAIN.
CC I-SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC I-SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC I-SIMILARITY: TO OFFER PROTEIN TYPE TOWATH DESCRIPTION FOR MATTICE
CO SIMILARITY: TO OFFER PROTEIN TYPE TOWATH DESCRIPTION FOR MATTICE
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CO TOWATH DESCRIPTION FOR THE FEBRET DESCRIPTION FOR MATTICE
CO
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PRINTS; PRO0109; TYRKINASE.
PROSITE; PS001007; PROTEIN_KIN
PROSITE; PS00109; PROTEIN_KIN
PROSITE; PS000109; PROTEIN_KIN
PROSITE; PS000791; RECEPTOR_T;
PROSITE; PS000791; RECEPTOR_T;
                                                    DOMAIN
TRANSMEM
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "An Eph-related receptor protein tyrosine kinase expressed in the developing mouse hindbrain."; Oncogene 7:2499-2506(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-C57BL; TISS MEDLINE; 93096484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
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EMBL; X57241; CAA40517.1; -.
EMBL; S57168; AAB25836.1; -.
HSSP; P00523; 2PTK.
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Chestier A., Wilkinson D.
                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
SIGNAL
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Mus musculus (Mouse).
Chordata;
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KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:98277;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
              20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ); PROTEIN_KINASE_ATP; 1.
); PROTEIN_KINASE_TYR; 1.
); PROTEIN_KINASE_DOM; 1.
); RECEPTOR_TYR_KIN_V_1; 1; RECEPTOR_TYR_KIN_V_2; 1
              Nieto
                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
POTENTIAL
EPHRIN TYPE-A RECEPTOR 4.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (BY SIMFIBRONECTIN TYPE-III (BY SIMFIBRONECTIN TYPE-III (BY SIMFIBRONECTIN TYPE-IN (BY SIMFIBRONECTIN 
                                                                                                                                                                                                                                                                                                                                                                                                     kinase; ATP-binding; Phosphorylation; pprotein; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       М.А.,
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Mus.
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М. -G
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THE CATALYTIC
                                                                                          SIMILARITY).
SIMILARITY).
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Best Local S
Matches 160
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (BRAIN-SPECIFIC KINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                     use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                 This
                                                                                                                                                                                                 J. Neurosci. Res. 37:129-143(1994).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
EPHRIN-A1, -A2, -A3, -A4 AND -A5.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                      Zhou R., Copeland T.D., Kromer L.F., Schulz N.T., "Isolation and characterization of Bsk, a growth factor receptor-like tyrosine kinase associated with the limbic system.";
J. Neurosci. Res. 37:129-143(1994).
                                                                                                                                                                                                                                                                                                                                                                                    EPHA5
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                                                                                                                                                                                                                                                                                          STRAIN=BALB/C; TI
MEDLINE; 94194581
                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               Eutheria;
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                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                 PROTEIN TYPOSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: BRAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLGTCKETF%LYIMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
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U07357;
                                                                                                                                                                                                                                                                                                                                                                                    OR EHK1 OR CEK7 OR BSK.
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Pred. No. 1.3e
30; Mismatches
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MISSING (IN SHORT ISOFORM).
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                                                                                                                                                  THE
                                              and
                                                                                                                                                  CATALYTIC
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Best Local S
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PRINTS; PRO0109; TYRKINASE.

PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00069; PFAM; PF00536; PFAM; PF01404;
                                                                                                                                                                                                                                               _RAT STANDARD; PRT; 1005 AA. EPBA5_RAT STANDARD; PRT; 1005 AA. P54757; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-NOY-1997 (Rel. 34, Last sequence update) 21-NOY-1997 (Rel. 35, Last annotation update) EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1). EPHAS OR EKH1 OR EHK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
SEQUENCE
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Maisonpierre P.C., Barrezueta N.X., Yancopoulos G.D.; "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosin kinase family with distinctive structures and neuronal expression."; Oncogene 8:3277-3288(1993).
                                                                                            STRAIN-SPRAGUE-DAWLEY; MEDLINE; 94067777.
                                                                                                                                                                                         Eutheria;
                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                      Rodentia;
                                                                                                                                                                                                       Metazoa;
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SAM; 1.
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97115 !
                                                                                                                                                                                 Sciurognathi;
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BY SIMILARITY.
EPHRIN TYPE-A RECEPTOR 5.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
                                                                                                                    TISSUE-BRAIN,
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Pred. No. 2.8e
35; Mismatches
                                                                                                                                                                                                         Craniata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54AD2DC864178214 CRC64;
                                                                                                                                                                                    Muridae;
                                                                                                                                                                                 Vertebrata;
ae; Murinae;
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                                             Eph receptor-like tyrosine
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72;
34;
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TARAMAN ARARAN ARAMAN ARAM
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PRINTS; PRO0109; TYKKINASE_ATP; FJ
PROSITE; PS00107; PROTEIN_KINASE_TYR; 1
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1
PROSITE; PS00109; RECEPTOR_TYR_KIN_V_1;
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_1;
PROSITE; PS001186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; T
MEDLINE; 95206467.
MEDLINE; OFART S., M1
 CONFLICT
CONFLICT
                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                          NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lassmann H., Steck A.J.;
"Expression and developmental regulation of Ehk-1,
Elk-like receptor tyrosine kinase in brain.";
Neuroscience 63:163-178(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X78689;
HSSP; P00523;
                                                      VARSPLIC
                                                                                                                                      VARSPLIC
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                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PR
ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED
SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: RECEPTOR FOR MEMBERS OF
                                                                                                                                                                                                                                                                                                                                                                                                      PF00041; fn3; 2.
PF00069; pkinase;
PF01404; EPH_lbd;
                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
  170
566
578
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677
683
709
266
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575
596
1005
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691
709
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PROTEIN_KINASE_DOM; 1.
RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miescher G.C., Honegger P.,
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                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
POTENTIAL
SPLICED FORMS).
SGSCCECGCGRASSLCAVAHPSLIW -
SPLICED FORMS).
D -> E (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
                                                                                                                                                                                                                                           ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                             VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCVCEKDYFR
RESDPTMACTR -> G (IN SPLICED FORMS)
RPPSAPRNAISNVNETSVFLEWIPPADTGGKDVSYYLICK
KCNSHAGVCEECGGHVRYLPQQIGLKNTSVMMADPLAHTNY
TFEIEAVNGVSDLSPGTRQYVSVNVTTNQAA -> T (IN
                                                                                                                                                 GRRRTQGRGGG ->
SPLICED FORMS)
                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                               kinase; ATP-binding; Phosphorylation;
oprotein; Signal; Alternative splicing
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Best Local S
Matches 150
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CONFLICT
CONFLICT
SEQUENCE
                         between
the Euro
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JULT-1996 (Rel. 36, Last annotation update)
15-JULT-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN-
KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-
TYROSINE KINASE HEK7).
EPHAS OR EHK1 OR HEK7.
                                                                                                                                                                                                            "cDNA cloning and tissue distribution protein-tyrosine kinases."; Oncogene 10:897-905(1995).
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                        ++
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                                                                                                                                                                                                                                                Basu R., Welcher A.A.;
                                                                                                                                                                                                                                                                                                                                                                            Eutheria;
                                                 This
                                                                                                                                                                                                                                                         MEDLINE; 95206782.
Fox G.M., Holst P.
                                                                                                                                                                                                                                                                                   TISSUE-BRAIN,
                                                                                                                                                                                                                                                                                            SEQUENCE OF 25-1037
                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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          s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                           SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE
ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESS
                                                                                                                                                             EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                             FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEEIGEVDENYAPIHTYQVCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                G.C.;
                                                                                                                                                                                                                                                                                                                                                                            Primates; Catarrhini;
                                                                                                                                                                                                                                                          Holst P.L.,
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708
979
1005
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                                                                                                                   ALMOST EXCLUSIVELY EXPRESSED
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Pred.
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-> I (IN REF. 2).
-> I (IN REF. 2).
-> I (IN REF. 2).
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                                                                                                                                                                                                                                                        Lindberg R.A.,
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ons on its in no way commercial
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Matches
MOUSE STANDARD; PRT; C61772; Q61773; Q61774; Q61505; Q61772; Q61773; Q61774; Q61505; Q61772; Q61773; Q61774; Q61505; Q61772; Q61773; Q61774; Q61505; Q61772; Q6173; Created) Q1-NOV-1997 (Rel. 35, Last sequence update) Q1-NOV-1997 (Rel. 35, Last annotation update) Q1-NOV-1997 (Rel. 35, Last annotation update) Q1-NOV-1997 (Rel. 35, Last annotation update) Q1-NOV-1997 (Rel. 35, Last sequence update) Q1-NOV-1997 (Rel. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
PROSITE; PS001186; EGF_2; UNKNOWN_1.
PFAM; PF00041; fn3; 2.
PFAM; PF000595; PK1nase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_1bd; 1.
Transferase; Tyrosine-protein kinase; AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0014; FY PRINTS; PRO0109; TY PROSITE; PS00107; PROSITE; PS00109; PS00109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X95425;
EMBL; L36644;
HSSP; P00523;
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CARBOHYD
CARBOHYD
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SIGNAL
CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
BINDING
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                                                                                                                                             VNHSVTDEPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLGTCKETFNMYYFESDDQNGRNIKENQYIKIDTIAADESFTELDLGDRVMKLNTEVRDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEEIGEVDENYAPIHTYQVCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPG 142
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AAA74245.
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3; TYRKINASE_ATP; 1.
77; PROTEIN_KINASE_TYR; 1.
109; PROTEIN_KINASE_DOM; 1.
11; PROTEIN_KINASE_DOM; 1.
90; RECEPTOR_TYR_KIN_V_1; 1
91; RECEPTOR_TYR_KIN_V_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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573
1037
1037
936
689
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264
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436
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619
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
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Pred. No. 1.2e
95; Mismatches
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ); DB 1;
1.2e-71;
nes 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ing; Phosphorylation;
Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.
PROSITE; PS001791; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS001791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS01186; SAM; 1.
PFAM; PF000401; fin3; 2.
PFAM; PF00056; PAM; 2.
PFAM; PF00056; SAM; 1.
PFAM; PF00556; SAM; 1.
PFAM; PF00556; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing
                                                     DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ciossek T., Millauer B., Ullrich A.;
"Identification of alternatively spl
MDK1, a novel receptor tyrosine kina
nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                         MGD; MGI:95276; EPHA7.
PRINTS; PRO0014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 96081374.

Ellis J., Liu Q., Breitman M., Jenkins N.A., Gilbert D.J., Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling Fletcher F.A., Ziegler S.F., Rogers J.H.; "Embryo brain kinase: a novel gene of the eph/elk receptor kinase family."; Mech. Dev. 52:319-341(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eutheria; Rodentia; Sciurognai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 431-998 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 10:97-108(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDK1.

MDK1.

MDK1.

IN SMERTYO. IN ADULT,
EXPRESSION RESTRICTED TO HIPPOCAMPUS, TESTIS AND SPLEEN.
EXPRESSION RESTRICTED TO HIPPOCAMPUS, TESTIS AND SPLEEN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA.
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BI EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE BHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (MDK1, MT ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN (MDK1, MT MDK1-2, MDK1-1, AND MDK1-T2) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT SPLICING OF THE SAME GENE.
                                                                                                                                                                                                                                                                                                                                                                                                ; X79082; CAA55687.1; -..; X79083; CAA55688.1; -..; X79084; CAA55689.1; -..; X81466; CAA57224.1; -..; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V.A., AND ALTERNATIVE TISSUE-BRAIN;
     998
556
577
998
537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                     Glycoprotein;
POTENTIAL.
EPHRIN TYPE-A RECEPTOR 7.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FROTEIN KINASE.
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Mus.
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murine
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protein-tyrosine kinases.";

Loncogene 10:897-905(1995).

Concogene 10:897-905(1995).

Concogene
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Best Local S
Matches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7_HUMAN
EPA7_HUMAN
Q15375;
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                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.11
KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3)
TYMOSINE KINASE HEKIL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
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                                                                                                                                                                                                                                                 Fox G.M., Holst P.L.,
Basu R., Welcher A.A.;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                      TYROSINE KINASE HEK11).
EPHA7 OR EHK3 OR HEK11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                      TISSUE-BRAIN;
MEDLINE; 95206782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
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MISSING (IN ISOFORM MDK1-T1).
FKEPGTKTYIDPETYEDPNRAVHQFAK -> S
EKYGHNKKWMLASCSRL (IN ISOFORM MDK1-T2).
MISSING (IN ISOFORM MDK1-T2).
Y > H (IN REF. 2).
                                                                                                                                                                                                                                                                   H.T.,
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Pred. No. 2.2e
86; Mismatches
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81C5538E15AEA2FA CRC64;
                                                                                                                                                                                                                                                                 Lindberg
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SIMILARITY).
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I ISOFORM
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PRINTS; PRO0109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KIN

PROSITE; PS00109; PROTEIN_KIN

PROSITE; PS00109; RECEPTOR_TIN

PROSITE; PS00790; RECEPTOR_TIN

PROSITE; PS00791; RECEPTOR_TIN

PROSITE; PS00791; RECEPTOR_TIN

PROSITE; PS001186; EGF_2; UNKN

PROM; PF00041; fn3; 2.

PFAM; PF00069; PKINASE; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF00536; SAM; 1.
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3).
EPHA7 OR EHK3 OR EHK-3.
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PROTEIN_KINASE_TYR; 1.

PROTEIN_KINASE_DOM; 1.

RECEPTOR_TYR_KIN_V_1; 1.

PRECEPTOR_TYR_KIN_V_2; 1
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69.58;
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POTENTIAL.
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ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479B9CA0D2BB06EB CRC64;
                                                                                                                                                                                                                                                         998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                      277
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Query Match 71.4
Best Local Similarity 69.4
Matches 155; Conservative
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CARBOHYD
VARSPLIC
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ACT_SITE
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SIGNAL
CHAIN
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[1]
                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                 PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE;
                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;

PROSITE; PS0071186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U21955;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         member of the Eph receptor tyrosine kinase Oncogene 10:1573-1580(1995).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE I
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ID N.Y., Goldfarb M., Yancopoulos G
"Identification of full-length and
                                                               SEQUENCE
                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U21954;
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                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
SPLICING, THE TRUNCATED FORM LACKS THE KINASE DOMAIN. THE LONG
FORM IS MORE WIDELY EXPRESSED IN THE EMBRYO.
TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.
SIMILARITY: TO OTHER PROTEIN-TYPOSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN
PROTEIN TYROSINE PHOSPHATE.
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Rodentia;
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                                                              998
                                                                                      Tyrosine-protein
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AAA86831.1; -.
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           71.4%;
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POTENTIAL.
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Score 856.5;
Pred. No. 2.86
7; Mismatches
                                                           FKFPGTKTYID -> SLVTI
ISOFORM).
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                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                      BY SIMILARITY.
PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                    FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILAR
                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                      EPHRIN TYPE-A
EXTRACELLULAR
                                                                                                                                                                                                                                                                                       kinase; ATP-binding; Phosphorylation;
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les 28;
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Rattus.
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Search completed: May 9, 2000, 22:32:06 Job time: 2397 sec

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	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31
	82.5	84.5	85.5	86	87.5	89.5	241	369.5	460	466	478	478	539	541.5	569.5
	6.9	7.0	7.1	7.2	7.3	7.5	20.1	30.8	38.3	38.8	39.8	39.8	44.9	45.1	47.5
	369	865	347	919	788	668	1122	1019	1006	987	987	987	984	952	849
	ν	N	N	N	N	N	ν	N	N	N	N	N	Ь	N	N
	в70220	H71447	T34131	T29581	I51530	T05803	T42400	T13039	JC5526	A54092	I48652	I48953	A34076	I50612	150617
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ALIGNMENTS

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C.Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea C.Reywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas F;1-20/Domain: signal sequence *status predicted <SIG>
F;21-983/Product: protein-tyrosine kinase hek *status experimental <MAT>
F;542-565/Domain: transmembrane *status predicted <TMM>
F;542-565/Domain: transmembrane *status predicted <TMM>
F;619-885/Domain: protein kinase homology <KIN>
F;627-635/Region: protein kinase ATP-binding motif
F;232,337,391,404,493/Binding site: carbohydrate (Asn) (covalent) *status predicted
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A;Residues: 1-983 <WIC>
A;Cross-references: GB:M83941; NID:g183931; PIDN:AAA58633.1;
A;Cross-references: GB:M83941; NID:g183931; PIDN:AAA58633.1;
A;Experimental source: pre-B-cell leukemia cell line LK63
A;Note: sequence extracted from NCBI backbone (NCBIP:86627)
A;Accession: B38224
RESULT 2
A45583
receptor tyrosine kinase Mek4 - mouse
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A; Residues: 21-39; 810-860 <WI2>
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R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.

New Biol. 3, 769-778, 1991

A;Title: Identification of a new eph-related receptor tyrosine kinase gene f A;Reference number: A45583; MUID:92031278

A;Accession: B4583

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-983 < SAD-
A;Cross-references: GB:M68514; NID:9454809; PIDN:AAA48666.1; PID:9211447
A;Cross-references: GB:M68514; NCBI backbone (NCBIN:62405, NCBIP:62411)
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein F;619-885/Demain: protein kinase homology < KIN>
F;627-635/Region: protein kinase homology < KIN>
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C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A45583
R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A;Title: Identification of a new eph-related receptor tyrosine kinase gene from A;Reference number: A45583; MUID:92031278
A;Reference number: A45583; MUID:92031278
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-983 <SAND
A;Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A;Cross-reference extracted from NCBI backbone (NCBIN:62398, NCBIP:62401)
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type [III C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein F;619-885/Domain: protein kinase ATP-binding motif
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C;Species: Gallus
C;Date: 22-Apr-1993
C;Accession: B45583
C;Accession: FG; Pa
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;Species: Gallus gallus (chicken)
;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994
;Accession: B45583
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VLGTCKETFNLYYMESDDDHLAKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEVREV
                           VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                  WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
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Pred. No. 3.2e
2; Mismatches
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Pred. No. 8.4e-96;
5; Mismatches 6;
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A;Cross-references: GB:L36645;
C:Genetics:
                                                                                                                                          receptor protein-tyrosine kinase - human (Species: Homo sapiens (man) C:Date: 29-May-1998 #sequence_revision 29-May-1998 C:Accession: I78844 R:Fox, G.M.: Holst, P.L.: Chute, H.T.: Lindberg, R. Oncogene 10, 897-905, 1995 A:Title: cDNA cloning and tissue distribution of fi A:Reference number: I58351; MUID:95206782
A;Gene: HEK8
C;Superfamily: protein-tyrosine k
F;619-885/Domain: protein kinase
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A;Residues: 1-948 <MAI>
A;Cross-references: EMBL:S68030
C;Superfamily: protein-tyrosine kinase, receptor type C;Keywords: ATP; transmembrane protein
F;628-936/Domain: protein kinase homology <KIN>
F;636-644/Region: protein kinase ATP-binding motif
                                                                                   A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-986 <RES>
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Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members
A;Title: Ehk-1 and Ehk-2: MUID:94067777
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R; Maisonpierre,
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995
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A; Accession: S51605
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74.0%;
                                                                     NID:g551613; PIDN:AAA74246.1;
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Pred. No. 2.3e
31; Mismatches
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A;Gene: Pag
C:Superfamily: protein-tyrosine kinase, receptor ty
C;Keywords: ATP; transmembrane protein
F;618-884/Domain: protein kinase homology <KIN>
F;626-634/Region: protein kinase ATP-binding motif
            protein-tyrosine kinase (EC 2.7.1.112) C;Speckes: Mus musculus (house mouse) C;Date: 19-Nov-1997 #sequence_revision C;Accession: $78059; $30505; I58366 R;Charnay, P.
                                                                            RESULT
S78059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor tyrosine kinase - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 C;Accession: I51549 R;Winning, R.S.; Sargent, T.D. Mech. Dev. 46, 219-229, 1994
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A;Reference number: IS1549; MUID:95001564
A;Accession: IS1549
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A; Residues: 1-985 <WIN>
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No. 1.6e-73;
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1.6e-74;
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C;Superfamily: protein-tyrosine kinase, recept (Keywords: ATP; transmembrane protein F;512-778/Domain: protein kinase homology <KI F;520-528/Region: protein kinase ATP-binding F;801-868/Domain: SAM homology <SAM>
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A; Residues: 1-877 <RES>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                  brain-specific kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #
C;Accession: 148967
R;Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz,
J. Neurosci. Res. 37, 129-143, 1994
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A; Residues: 1-31,55-986 <GIL>
A; Cross-references: EMBL: X65138
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A;Title: An Eph-related receptor protein tyrosine A;Reference number: S30496; MUID:93096484
A;Accession: S30505
                                                                                                                                                                                                                                                   A; Reference number: I48967; A; Accession: I48967
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A; Accession: S78059
A; Molecule type: mRNA
A; Residues: 1-986 < CHA>
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p autophosphorylation; glycoprotein; phosphoprotein;
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68.3%;
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, M.A.; Frain, M.; Mattei, M.G.; Chestie
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Similarity

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receptor tyrosine kinase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Accession: $47489
R;Taylor, V.; Pfarr, S.; Miescher, G.C.; Honegger, P.; Breitschopf, H.; Lassmann, H.; Submitted to the EMBL Data Library, April 1994
A;Description: Expression and developmental regulation of EHK-1, a neuronal ELK-like re
A;Reference number: $47489
A;Reference number: $47489
A;Accession: $47489
A;Cassion: $47489
A;Residues: 1-898 <TAY>
A;Cross -references: EMBL:X78689; NID:9531543; PIDN:CAA55357.1; PID:9531544
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Keywords: ATP; transmembrane protein
F;568-834/Domain: protein kinase homology <KIN>
F;576-584/Region: protein kinase ATP-binding motif
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                                                                                                                                               VNHSVTDDPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ
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                                                                                                                                                                                                                                                                                                                  Score 866.5; |
Pred. No. 5.1e
35; Mismatches
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                                                                      #text_change
                               Eph receptor-like
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Best Local S
Matches 150
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Matches 150
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receptor-like tyrosine kinase Ehk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 *sequence_revision 21-Jul-1995 *te
C;Accession: $51604
R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G
Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph
A;Reference number: $49015; MUID:94067777
A;Accession: $51604
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-981 <MAI>
A;Cross-references: EMBL:$68029
A;Note: the authors translated the codon GAC for resid
C;Reywords: ATP; transmembrane protein
C;Reywords: ATP; transmembrane protein
E;651-917/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-893 <mAI>
A; Residues: 1-893 <mAI>
A; Cross-references: EMBL:S58028
A; Cross-references: EMBL:S58028
C; Superfamily: protein tyrosine kinase, receptor C; Superfamily: protein tyrosine kinase, receptor C; Keywords: ATP; transmembrane protein F; 563-829/Domain: protein kinase homology <KIN>
F; 571-579/Region: protein kinase ATP-binding moti
                                                                                                                                                                                                                                   VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
||:| :||:|:|| |||||||||| | |||||:
| VNHSVTDDPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ
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                      VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                GPVNKKGEYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                       GLGTCKETFNMYYFESDDENGRNIKDNQYIKIDTIAADESFTELDLGDRVMKLNTEVRDV
                                                                                                                                                                          VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
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VNHSVTDDPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ
                                                                         GPLSKKGFYLAFQDVGACIALVSVRVYYKKCPSVVRHLAVFPDTITGADSSQLLEVSGSC
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150; Conservative
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67.9%;
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                                                                                                                                                                                                                                                                                                                 Score 863.5;
Pred. No. 1.1e
36; Mismatches
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Pred. No. 9.5e
36; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-Jul-1995 #text_change
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.5e-71;
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type eph; fibronectin
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67.98;

2e-70;

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RESULT 12

$49015

receptor tyrosine kinase Ehk-1 - rat
receptor tyrosine kinase Ehk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C;Accession: $49015; $51602
R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Accession: S49015; MUD:94067777
A;Recession: S49015
A;Recession: S49015
A;Residues: 1-1005 <MAI>
A;Residues: 1-1005 <MAI>
A;Cross-references: EMBL:S68024
A;Molecule type: mRNA
A;Residues: 1-305; G', 359-1005 <MA2>
A;Status: preliminary
A;Residues: 1-305; G', 359-1005 <MA2>
A;Cross-references: EMBL:S68026
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III
C;Keywords: ATP; transmembrane protein
F;675-941/Domain: protein kinase homology <KIN>
F;683-691/Region: protein kinase homology <KIN>
F;683-691/Region: protein kinase ATP-binding motif
                                                                                        receptor protein-tyrosine kinase - human (fragment)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C:Accession: I78843
R:FOX, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, Oncogene 10, 897-905, 1995
A:Title: cDNA cloning and tissue distribution of five human EPH-like receptce A:Reference number: I58351; MUID:95206782
A;Status: preliminary; translated from GB/EMBI/DDBJ
A:Status: preliminary; translated from GB/EMBI/DDBJ
A:Molecule type: mRNA
A:Residues: 1-991 <RES>
A:Cross-references: GB:L36644; NID:g551611; PIDN:AAA74245.1; PID:g551612
C:Genetics:
    A; Gene:
C; Superf
F; 627-89
F; 916-98
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C;Superfamily: pro
F;627-893/Domain:
F;916-982/Domain:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC 179
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                                                 protein-tyrosine kinase,
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    protein kinase
SAM homology <8
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       SAM>
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                        homology
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Pred. No. 1.1e-70;
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                           receptor type
gy <KIN>
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                                                 eph;
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                                              fibronectin type
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Query Match

Score

860.5;

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2

Length

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A; Experimental source: embryo
A; Experimental source: embryo
C; Comment: This enzyme plays a regulatory role during neural c; Comment: bris enzyme plays a regulatory role during neural c; C; Keywords: brain; phosphotransferase
F; 1-30/Domain: signal sequence #status predicted <SIG>F; 31-605/Product: receptor tyrosine kinase Ebk-tdl #status pre F; 31-548/Domain: extracellular #status predicted <EXT>F; 31-548/Domain: fibronectln type III repeat <FNI>F; 441-534/Domain: fibronectln type III repeat <FNI>F; 441-534/Domain: transmembrane #status predicted <TMM>
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developmental kinase 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-U1-1996 #sequence_revision
C;Accession: I48612; S51741
R;Ciossek, T; Millauer, B.; Ullrich, A
Oncogene 9, 97-108, 1995
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A;Cacession: 148612
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21-JUN-1991; AU-006841.
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BOYD AD, SIMPSON R, WARD LEAST REPER PRINTER PRINTER
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Claim 6; Fig 1; 58pp; English.

This sequence represets human eph/elk-like kinase (HEK). HEK is expressed in both pre-B cells and T cell lines and in a number of tumours of human origin, eg. lymphoid tumours LKG3, Lila-1 and JM, and the epithelial tumour HeLa. This receptor-type thymidine kinase (TK) and/or its ligands are useful as agents in modulation of the
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Cek4; Eph; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 85-89; 129pp; English.
Probes derived from the EPH-related PTMs Cek4 (090659) and Ce (090660) were used to isolate novel cDNA clones (090652-58, 090661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues and also in the adult brain and retina. Seguence 983 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production and/or function analogues have activity in cellular responses such as Sequence 983 AA;
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Best Local S
Matches 159
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W83148;
                                  domain
                                                                                                domain
                                                                                                                                                              domain
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                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-1999
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US5843749-A.
01-DEC-1998.
06-JUN-1995; 469537.
17-MAR-1995; US-406247.
17-MAR-1995; US-706247.
26-JUL-1991; US-736559.
28-OCT-1993; US-7469537.
(REGE-) REGENERON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat receptor tyrosine kinase Ehk-2.
Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-:
neurotrophin activity; trkB; protto-oncogene;
binding protein; BDNF; NT-3; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 21; 194pp; English.

The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding prof Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence represents rat Ehk-2. Sequence 948 AA;
                                                                                                                                                                  differentiation.
                                                                                                                                                                           Protein tyrosine-kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maisonpierre PC, M
WPI; 99-044584/04.
N-PSDB; V70208.
                                                                                                                                                                                                                    14-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                   236 VKSSEERDTPKLYCGADGDWLVPLGRCICTTGYEE
                                                                                                                                                                                                                                                                                                                                                                                                  WEEISGYDEHYTPIRTYQYCNYMDHSQNNWLRTNWYPRNSAQKIYYELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                                                                                  VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLGTCKETFTLYYIESDESHGTKFKPSQYIKIDTIAADESFTQMDLGDRILKLNTEVREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WDAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKFTLRDCNSIPW 115
                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 74.(59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor
/label=
571. .98
/label=
                                                  /label=
20. .547
/label=
548. .57
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                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                     Protein;
                                                   .570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.2%;
74.0%;
                    . 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine
                                  Transmembrane_domain
                                                                 Extracellular_domain
                                                                                                  Sig_peptide
                                                                                                                                                                                                     bpTK7
Intracellular_tyrosine-kinase_domain
                                                                                                                                                                                  PTK;
                                                                                                                                                                                                                                                     986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 914.5; DB 1
Pred. No. 1.5e-88;
1; Mismatches 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                  bpTK7; agonist; cell growth;
                                                                                                                                                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                     270
                                                                                                                                                                                                                                                                                                                                                                    214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Ehk-2;
tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
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RESULT
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Best Local S
Matches 162
                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1995.
14-APR-1995; U04681.
15-APR-1994; US-229509.
(AMGE-) AMGEN INC.
(AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agonist antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain useful for studying, and therapeutic modulation of, cell growth and differentiation Disclosure; Page 95-99; 125pp; English.

DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify novel pTK genes. The bpTKs, bpTK1, bpTK2, bpTK3, bpTK4, bpTK5 and bpTK7 (R85924-28 and R85935, respectively) are expressed in human brain tissue and show homology to known pTKs. A full-length sequence for bpTK7 (R85956) was also obtd. bpTK7 can be used to design drugs that modulate pTK activity.
4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK6 HEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (702946-49) from a human foetal by cDNA library. HEK7 and HEK8 (T02946-49) from boology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. Recombinant HEK8 receptors (or their soluble extracellular domains) are produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPH-like receptor protein tyrosine kinase HEK8.
EPH-like receptor protein tyrosine kinase; PTK; HEK8;
human eph-like kinase; therapy; diagnosis; vector; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood
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12-OCT-1995.
04-APR-1995; U04228.
04-APR-1994; US-222616.
                                                                                                                                                                                                                                                                           New nucleic acid encoding and related vectors, host
                                                                                                                                                                                                                                                                                                                               N-PSDB; T02948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO
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Agonist antibodies which
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Bennett BD, Goedd
                                                                                                                                                                                                                                                  diagnostically
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95-366160/47.
                                                                                                                                                                                                                                                                                                                                                        3M, Jing S,
95-373799/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162;
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                                                                                                                                                                                           Page 62-65; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                             id encoding EPH-like receptor tyrosine kinase(s) ctors, host cells, proteins, antibodies etc., used and therapeutically to modulate receptor activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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73.3%;
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Pred.
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No. 1.4e-87;
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                                                                                                                                                                                                                                               activation
                                                                                                           HEK5, HEK7,
I following
an foetal brain
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Best Local S
Matches 162
                                                                                                                                                                                                                                                                                                (ZHOU/) ZHOU N. (ZHOU/) ZHOU N. W. KIOMET LF, Schulz NT, W. WPI; 98-541751/46.
injuries, neurinia, c
schizophrenia, c
                        Claim 1; Fig 2; 72pp; English.

Claim 1; Fig 2; 72pp; English.

The present sequence represents mouse Bsk, which is a receptor-like tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in Bsk nucleic acid probes, which can be used in detecting alterations in the level of Bsk messenger-RNA (mRNA) in biological samples isolated from a mammal afflicted with a disease, such as neurodegenerative diseases or disorders and neoplasms. The nucleic acid sequence can also be delivered into the limbic system of patients with limbic system neurodegenerative disease, disorder or injury, to promote or enhance limbic system neuron regeneration or growth. Such neurodegenerative disease, viral infections, bacterial infections, brain injuries, neoplastic conditions, Alzheimer's disease, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression cells, and
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11-JUN-1996; 673789.
04-JAN-1994; US-177812
11-JUN-1996; US-673789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neoplasm; neurodegenerative disease; limbic system neuron regeneration; chromosomal abnormality; degenerative growth; development disorder; viral infection; bacterial infection; Alzheimer's disease; epilepsy;
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                                                                                                                                                                                                                                                  Isolated nucleic acid sequence encoding protein - used nucleic acid probes, used in detecting alterations in 1 messenger-RNA in biological samples isolated from mamma
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ZHOU R.
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Pred. No. 1.4e-87;
0; Mismatches 28;
                   cerebral
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Best Local S
Matches 151
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US5843749-A.
01-DEC-1998.
06-JUN-1995; 469537.
17-MAR-1995; US-406247.
26-JUL-1991; US-736559.
28-OCT-1993; US-14492.
06-JUN-1995; US-469537.
(REGE-) REGENERON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins

Example: Fig 22: 194pp: English.

The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins: Ror-1: Ror-2: Ehk-1: and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence represents rat Ehk-1.

Sequence 1005 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maisonpierre PC, Ma
WPI; 99-044584/04.
N-PSDB; V70207.
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Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection; neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor; binding protein; BDNF; NT-3; diagnosis.
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Pred. No. 1.7e-83;
"" "" amatches 34;
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Pred. No. 2.1e-83;
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AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in treatment and diagnosis of neuronal disorders and angiogenesis-related conditions.

The angiogenesis-related conditions.

Example 1; Page 50-53; 75pp; English.

Example 1; Page 50-53; 75pp; English.

Rat REK7 (R97853) is an eph-related tyrosine kinase receptor, for which AL-1 (see also W97854) is a ligand. Its amino acid sequence which AL-1 (see also W97854) is a ligand. Its amino acid sequence was deduced from a cDNA clone (T18893) isolated from a hippocampal cDNA library. An REK-19G fusion was used to screen cultured cell lines for surface expression of REK7-binding activity. Primers (see also T44382-83) based on peptide sequences (R97885-59) of isolated ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human footal brain cDNA library, leading to the isolation of AL-1 cDNA crimages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.1
Best Local Similarity 68.3
Matches 151; Conservative
    R85090 standard; Protein; 991 AA. R85090; R850900; R85090; R85090; R850900; R850900; R850900; R850900; R850900000; R8509000; R8509000; R85090000000000000000000000000000000000
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27-OCT-1994; US-330128.
07-JUN-1995; US-486449.
(GETH) GENENTECH INC.
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09-MAY-1996.
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Rat REK7 eph-related tyrosine kinase receptor.
REK7; eph-related tyrosine kinase receptor; AL-1; ligand;
neurotrophic factor; neuropathy; anglogenesis; therapy; diagnosis.
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05-JAN-1997
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sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNHSVTDDPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ
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58. .462
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58. .928
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RESULT NO 3422 ID WO 3422 WO DE MY CON WO CO
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Claim 18; Page 14-57; Page 14-57;
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Best Local S
Matches 150
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14-APR-1995; U04681.
15-APR-1994; US-229509.
(AMGE-) AMGEN INC.
FOX GM, Jing S, Welcher A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse developmental kinase 1 MDK1 T1.

Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase; RTK; signal transduction; probe; diagnosis; gene therapy;
       misc_difference
                                                                                                                                         modified_site
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95-373799/48.
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                                                                      410. .41
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555. .57
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                                                                                                                                      el= N-glycosylation_site
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                                                                                                  N-glycosylation_site
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03-JAN-1996; US-368776.
03-JAN-1995; US-368776.
(PLAC) MAX PLANCK GES F
(SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 109-111; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting identified 2 truncated versions, MDKI T1 (W03422) and MDKI T2 (W03423), of the novel mouse developmental kinase 1 (MDKI) (see als W03423), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from CDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDKI, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential agents useful for treatment of diseases characterised by abnormal signal transduction.
  WO9621013-A1
                        misc_difference
                                                                                           modified_site
                                                                                                                                       peptide
                                                                                                                                                                                        RTK;
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                                                                                                                                                               Mus sp.
                                                                                                                                                                          neurodegeneration; neuroproliferation;
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                                                                                                                                                                                   e developmental kinase 1 MDK1 T2.
e developmental kinase 1; MDK1 T2; receptor tyrosine kinase;
signal transduction; probe; diagnosis; gene therapy;
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343. .345
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555. .57
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                                                                   el- N-glycosylation_site
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                        . 626
                                             יבי N-glycosylation_site
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            "product
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11-JUL-1996.
03-JAN-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES F
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CDNA cloning using adult mouse brains and Northern blotting identified 2 truncated versions, MDK1 T1 (W03422) and MDK1 T2 (W03423), of the novel mouse developmental kinase 1 (MDK1) (see als W03423), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential agents useful for treatment of diseases characterised by abnormal signal transduction.
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New mouse development kinase 1 gene - use new mouse development of abnormalities
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11-NOV-1996 (first entry)
Mouse developmental kinase 1; MDK1; receptor tyrosine
Mouse developmental kinase 1; MDK1; receptor tyrosine
signal transduction; probe; diagnosis; therapy;
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03-JAN-1996; US-368776.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
(SUGE-) SUGEN INC.
Clossek T, Millauer B, Ullrich A;
WPI; 96-333988/33.
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Key
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VSSAEEEAENSPRMHCSAEGEWLVPIGKCICKAGYQQKGDTCE 277
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555. .57
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64..66
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Mouse developmental kinase 1 (MDKI) (W03421) is a new member of the ceck/eph family of receptor tyrosine kinases (RTKs). Its amino cack sequence was deduced from a cDNA clone (T32960) isolated from mouse embryo and adult brain libraries. The distinct patterns of MDKI expression during mouse development suggest an important role for MDKI in the formation of neuronal structures. MDKI may be obtd. by expression in host cells. It can be used in methods for the diagnosis of diseases characterised by abnormality in a signal transduction pathway, such as neuroproliferative or neurodegenerative disorders or cancer, to screen for (ant)agonists, and to raise antibodies.
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Best Local Similarity
Matches 156; Conserv
           Claim 18; Page 71-75; 133pp; English.

4 Novel human EPH-11ke receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (T02946-49) from a human foetal brain cDNA library. HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-1ike receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-1ike receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced by
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N-PSDB; T32960.
New mouse development kinase
New mouse development of ak
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                                                                                                                                                      New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., us diagnostically and therapeutically to modulate receptor activa
                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9528484-A1.
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EPH-like receptor protein tyrosine kinase; PTK; HEK11;
human eph-like kinase; therapy; diagnosis; antibody; vector.
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                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
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15-APR-1994; US-229509
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. No. 1.8e-82;
ismatches 28;
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Matches 128
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Best Loc
Matches
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07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER R
(LJOL-) LA JOLLA CANCER R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HEK receptors, or therapeutically to modulate the activation of cell-associated receptors.

Sequence 998 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prognosis.
Gallus sp.
WO9515375-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 92-96; 129pp; English.

Probes derived from the EPH-related PTKs Cek4 (090659) and (090660) were used to isolate novel cDNA clones (090652-58, 090661-62) from chicken embryo and embryonic brain librarie Sequence 995 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R75712 standard; Protein;
R75712;
11-NOV-1995 (first_entry)
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08-JUN-1995.
07-SEP-1994; U10140.
07-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RE.
Pasquale EB, Sajjadi FG;
WPI; 95-215256/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                         R75709 standard;
R75709;
11-NOV-1995 (fir
                                                                                                                                                                                                                    Claim 11; Page 71-75; 129pp; English.

A cDNA clone encoding a novel variant of EPH-related PTK Cek5+ (290657), was isolated from a chick embryo library lambda gtl1. Cek5+ protein (R75709) contains a 16-amino insertion in the juxtamembrane domain, and be a result of alternative splicing. Cek5+ is exclusively expressed in sequence 1011 AA;
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Copyright (c) 1993 - 2000 Compugen
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017213	015832	034753	099544	Q9YR38	Q9YR39	077403	005459	028496	Q9Y667	Q9Y5P7	060993	Q83876	014237	023393	Q18228	Q59082	Q96725	Q66530	Q9YS14	Q9ZCV2	P71504	096993	Q83884	Q21794
_		034753 bacillus su	099544 paramesopod	Q9yr38 aleutian mi	Q9yr39 aleutian mi	077403 sciara ocel	005459 mycobacteri	arch	Q9y667 homo sapien		a	Q83876 norwalk vir	014237 schizosacch	O23393 arabidopsis	Q18228 caenorhabdi	Ω	european	Q66530 european br	Q9ys14 norwalk vir	Q9zcv2 rickettsia		O96993 heterodera	Q83884 norwalk vir	Q21794 caenorhabdi

ALIGNMENTS

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	POO523; 2PTK.		!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN	-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	AND IN THE PRONEPHRO	RAL ARCI	-)- TISSUE SPECIFICITY: LOCALIZED EXPRESSION IN A SUBSET OF NEURAL CREST AND NEURAL TISSUES IN EMBRYOS.	!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	TYROSINE PHOSPHATE.	TVBOCTNE - ADD + DE	SIMILARITY). MAY PLAY A ROLE IN THE DIFFERENTIATION OF CRANIAL	SASSAGE SEALS SANIA		essi	orio. A member of the Eph family of recentor tyrogine		TISSUE=NEURAL CREST;	SEQUENCE FROM N.A.	[1]		esobatrachia; Pipoidea; Pipidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;			U1-NOV-1999 (TREMBERGE: 12, Last annotation update) TYROSINE-PROTEIN KINASE RECEPTOR PAG PRECURSOR (EC 2.7.1.112)	(TrEMBLrel. 01, Last	01-NOV-1996 (TrEMBLrel. 01, Created)	Q91694 FRELIMINARI; FRI; 985 AA. Q91694;		OLT 1

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Best Local S
Matches 14
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091845;
01-NOV-1996 (TIEMBLIEL 0
01-NOV-1996 (TIEMBLIEL 0
01-NOV-1999 (TIEMBLIEL 0
01-NOV-1999 (TIEMBLIEL)
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 96125143.
XU Q., ALLDUS G., HOLDER N
"Expression of truncated S
segmental restriction of g
hindbrain.";
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; |
Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
DISULFID
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
SEQUENCE
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TRANSMEM
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PEAM; PEO
PEAM; PEO
PEAM; PEO
                                 +++
                                                                                                                                         Development 121:4005-4016(1995).

-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A SIMILARITY). REQUIRED FOR INTERACTIONS THAT RECIDENTITY OR MOVEMENT OF CELLS.
-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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PRINTS; PRO0014; FNTYPEIII.
Transferase; Tyrosine-protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYROSINE-PROTEIN KINASE
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| ||||::::||||||: | |
31 VTLLDSRSVQGELGWIASPLEG
             DEVELOPMENTAL STAGE: EXPRESSION OCCURS IN 73, R5 AND TRANS:
AT LOWER LEVELS IN R2.
AT LOWER LEVELS IN R2.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: TO OTHER PROTEIN-TYPOSINE KINASES IN THE CATALDOMAIN. BELONGS TO THE EPH FAMILY.
                                                                                                                        SUBCELLULAR LOCATION: TYPE I
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PF00069;
PF00536;
PF01404;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa;
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; SAM; 1.
; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                              a; Chordata; Craniata; Ven
Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR_TYR_KIN_V_2; 1.
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L.1; -
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01, Last sequence update)
12, Last annotation update)
RECEPTOR SEK-1 PRECURSOR (E)
                                                                                                                                                                                                                                                                    N., WILKINSON D.G.;
Sek-1 receptor tyrosine kinase disrupts
gene expression in the Xenopus and zebra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
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CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN (BY S
CYS-RICH.

FIBRONECTIN TYPE-III (BY SIM
FIBRONECTIN TYPE-III (BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (
POTENTIAL.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
ia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase; ATP-binding; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                    frog).
                                                                                                       ION OCCURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                     PROTEIN.
                                                                                                                                                                                              EPHRIN-A FAMILY
S THAT REGULATE
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                                                                                                                                                                                                                                                                                                                                                                                                                   Amphibia;
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                                                                                                       AND TRANSIENTLY
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SIMILARITY).
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                                 CATALYTIC
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013146;
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ACT_SITE
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CARBOHYD
CARBOHYD
SEQUENCE
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TRANSMEM
                                                       BOVENRAMP D.E., GREER P.;
BOVENRAMP D.E., GREER P.;
BOVENRAMP D.E., GREER P.;
"Novel Eph-family receptor tyrosine kinase is widely expressed in the "Novel Eph-family receptor system.";
developing zebrafish nervous system.";
Dev. Dyn. 209:166-181(1997).
-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A ROLE IN EARLY PATTERN FORMATION WITHIN THE DEVELOPING NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
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01-JUL-1997 (TrembLrel. 04,
01-NOV-1999 (TrembLrel. 12,
EPH-LIKE KINASE 1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase;
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_1bd;
                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra
Eukaryota; Metazoa; Chordata; Crania
Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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PRINTS; PROO014; FNTYPEIII.
                                                                                                                                                         Cyprinoidea;
                                                                                                                                                                                                ZEK1
                                                                                                                                                                                                          RECEPTOR
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                                                                                                                                      SEQUENCE FROM
                                                                                                                              EDLINE;
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                                                                                                                                                                                                                                                                                                                             1 VNLLDSKTIQGELGWISYPSHG
                                               SYSTEM.
CATALYTIC ACTIVITY:
         TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: WI
NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                      w
                                                                                                                                                                                                                                                                                                                 VTLLDSRSVQGELGWIASPLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P00523;
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PS00109; PROTEIN_KINASE_TYR; 1.
PS00790; RECEPTOR_TYR_KIN_V_1;
PS00791; RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                         Cyprinidae;
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OTHER
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63.6%;
                  WIDELY
                                                ATP
PROTEIN-TYROSINE KINASES
                                                                                                                                                         Rasborinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
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                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
(EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
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                                                                                                                                                                                                                                                                                                                                                       Score 79; DB
Pred. No. 0.00
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. v; 028DBBDA CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYROSINE-PROTEIN KINASE RE EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
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ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP
                                                                                                                                                       (Zebra danio).
Craniata; Vertebrata;
eostei; Ostariophysi; (
orinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (AUTO-) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase;
                                                                                                                                                                                                                                                                  PRT;
                  I MEMBRANE
EXPRESSED :
                                                PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
                                                                                                                                                                                                                                                                  981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                TYROSINE -
                                                                                                                                                                                                                                                                  ₽
                 E PROTEIN.
IN THE DEVELOPING ZEBRAFISH
                                                                                                                                                                                                                                                                                                                                                                 .00037
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                                                PROTEIN
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Best Local Similarity
Matches 13; Conser
                                                                                                            042422 PRELIMINANA,
042422;
01-JAN-1998 (TIEMBLrel. 05, Created)
01-JAN-1998 (TIEMBLrel. 05, Last sequence update)
01-JAN-1998 (TIEMBLrel. 12, Last annotation update)
01-NOV-1999 (TIEMBLREL. 12, Last annotation updat
EPH-LIKE RECEPTOR TYROSINE KINASE PRECURSOR (EC 2
                                                                                                                                                                                                                                                                                                VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                NP_BIND
DISULFID
BINDING
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DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZFIN; ZDB-GENE-990415-58; Zek1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FALSE_NEG.

PFAM; PF00069; pkinase; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
  MEDLINE; 98092111.

ARAUJO M., NIETO M.A.;

ARAUJO M., NIETO M.A.;

The expression of chick EphA7 during segmentation peripheral nervous system.";

Mech. Dev. 68:173-177(1997).

-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN EP-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE --
                                                                       SEQUENCE
                                                                                                Eukaryota;
                                                                                                       Gallus gallus (Chicken).
                                                              TISSUE-EMBRYO;
                                                                                      Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                     30
                                                                                                                                                                                                                                1 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                            ٠
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; U89295;
; P00523;
                                                                                                                                                                                                                    VTLLDSMSAPGDLGWEAYPSEG
                                                                      FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                Metazoa;
                                                                                      Galliformes;
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC60220.1;
2PTK.
 RECEPTOR FOR MEMBERS OF THE EPHRIN ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                      N.A.
                                                                                                                                                                                                                                                                                                 À,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYRKINASE.
                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                                109654
                                                                                                                                                                                                                                                             59.7%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotei
BY SIMI
                                                                                      Phasianidae;
                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                     ů.
                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (
                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                              Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
S -> N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPH-LIKE KINASE 1.
                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                            Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                -> N.
10D38182 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY
                                                                                                                                                                                                                                                      Mismatches
                                                                                      Phasianinae;
                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Immunoglobulin domain.
                                                                                                                                                                                                                                                              DB 13;
0.0067;
                                                                                                                              update)
(EC 2.7.1.112)
                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                     Length 981;
  FAMILY.
                                                                                                                                                                                                                                                     Indels
                                   0£
  ADP + PROTEIN
                                                                                      Gallus
                                                                                             Archosauria; Aves
                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY)
                                   the
                                   central
                                                                                                                               (TYROSINE-
                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                     Gaps
                                   and
                                                                                                                                                                                                                                                     0;
RESULT
ID 191571
ID 291571
ID 201571
OUT 00
DT 00
DT 00
DT 00
DT 00
DT 00
RN
RN
RX
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Query Match
Best Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00107; PROTEIN_KINASE_ATF; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF00069; PK1nase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF010404; EPH_Lbd; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y14271;
HSSP; P00523;
PROSITE; PS001
SEQUENCE;
                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
DISULFID
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                         Eukaryota;
Batrachia;
                                                                                                                             01-NOV-1996 (TremBLrel. 01, 01-NOV-1996 (TremBLrel. 01, 01-NOV-1999 (TremBLrel. 12, EPHRIN TYPE-B RECEPTOR XEK I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
SIGNAL
                                                                                                                                                                                                      Q91571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>:</u>
                               Xenopus.
                                                                                                                                                                                          Q91571;
                                                      Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Crania
Batrachia; Anura; Mesobatrachia; Pip
                                                                                                       XEK
                                                                                                                   KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0014; FNTYPEIII
                                                                                                                                                                                                                                                                             ^{3}_{3}
                                                                                                                                                                                                                                                                                              1 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SÜBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS
RESTRICTED TO PROSOMERES I AND 2 IN THE DIENCEPHALON AND ALL THE
REOMBOMERES IN THE HINDBRAIN DURING SEGMENTATION STAGES, LATER ON,
A SUPERIMPOSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION
OF SEVERAL AXONAL TRACTS. IN THE SOMITIC MESODERM, THE EXPRESSION
CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST
AND MOTOR AXONS THROUGH THE SCLEROTOMES.
SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC
SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                             VILLDSKAQQTELEWISSPPNG
                                                                                                                 RECEPTOR
 95215070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                              993
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Immunoglobulin domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAA74643.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                              ₽,
                                                                                                                 XEK).
                                                                                                                                                                                                                                                                                                                                                                                                                                        51.3%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                              111366
                                                                                                                                                                                                                                                                                                                                                   . 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
POTENTIAL.
                                                                                                                            , Created)
, Last sequence update)
, Last annotation update)
PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                              WW.
                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                             54
                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIBRONECTIN TYPE-III (FIBRONECTIN TYPE-III (FIBRONECTIN TYPE-III (FIBRONECTIN KINASE. ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
1; 6B6BFD17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPH-LIKE RECEPTOR TYROSINE KINASE. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                        PRT;
                                                                       Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                        Pipoidea;
                                                                                                                                                                                                                                                                                                                                                     NO.
                                                                                                                                                                                                        985
                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                            DB .
.26;
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                                                                                                                                                                                                                                                                                                                                                                                                              CRC32;
                                                                                                                                                                                                                                                                                                                                                                  13;
                                                        Pipidae;
                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                 Length 993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
                                                                                                                                                                                                                                                                                                                                      Indels
                                                        Xenopodinae;
                                                                       Amphibia;
                                                                                                                             (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain.
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RESULT
Q91735
ID Q9
AC Q0
DT 00
DT 00
DT 00
DT 00
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                                                                                                                                                                                                                     Matches
                                                                                                                                                                        Query Match
Best Local
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PROSITE; PS00107; PROTEIN_KINASE_ATF; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; FA
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF00036; PKINASE; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF001404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91735
Q91735;
Q1-NOV-1996
Q1-NOV-1999
                                                                                                                                                                                                                   NP_BIND
DISULFID
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I- DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID BLASTULA TRANSITION AND REAPPEARS AT LATE NEUTULATION. EXPRESSED AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC STACES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBIQUITOUSLY EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION I THE BRAIN, BRACHIAL ARCHES, TRIGEMILLA FACIAL GANGLION, AND THE RETINA OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.
--- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
--- SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE C2-TYPE DOMAIN.
--- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
EMBL, U14164; ARAP4488.1; --
                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PROO109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor;
                                                                                                                   24
                                                                                                                                      3 LLDSKTIQGELGWISYPSHG
                                                                                  σ
                                                                                                                   LMDTRTATAELGWTANPSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P00523; 2PTK.
                                                                                                                                                              l Similarity
10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
(TremBLrel. 01, Created)
(TremBLrel. 01, Last sequence update)
(TremBLrel. 12, Last annotation update)
-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tyrosine-protein
                                                                                                                                                                                                                                          48.7%;
50.0%;
                                                                                                                                                                                                                    110104
                                                                                                                                                                                                                                                                                                                                                                                                                                  otein kinase; ATP-binding; Phosphorylation;
Glycoprotein; Signal; Immunoglobulin domain.
POTENTIAL.
                                                                                                                   43
                                                                                                                                       22
                                                                                                                                                                                                                    ₹
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                                                                                                                                                                                                                                                                         ATP (BY SIMILAR
BY SIMILARITY.
ATP (BY SIMILAR
BY SIMILARITY.
                                                                                                                                                             4.
                                                                                                                                                            Score 58; DB 13;
Pred. No. 0.76;
4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
CYS-RICH.
                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                            EPHRIN TYPE-B RECEPTOR XEK. POLY-LEU.
                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                               FIBRONECTIN TYPE-III.
                                                           PRT;
                                                                                                                                                                                                                   2416A8F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEMBRANE PROTEIN.
ALLY EXPRESSED, IT DECREASES AT MID
ANTICLE TO ANTICULATION. EXPRESSED
                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
                                                          974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FALSE_NEG
                                                          ₿
                                                                                                                                                                                                                    CRC32;
                                                                                                                                                            6,
                                                                                                                                                                                 Length 985;
                                                                                                                                                            Indels
                                                                                                                                                            0
                                                                                                                                                           Gaps
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RESULT
043477
ID 04
AC 04
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                                                                                                                                            Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                        EMBL; L43520; AAA93526.1; -.
HSSP; P005523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF00536; SAM; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
043477;
                                                                                                                                           ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                    NP_BIND
                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                           Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 96068901.

SCALES J.B., WINNING R.S., RENAUD C

"Novel members of the eph receptor
during Xenopus development.";
Oncogene 11:1745-1752(1995).

-i- FUNCTION: RECEPTOR FOR MEMBERS
                                                                                                                                                                                                                                                                                        CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0109; TYRKINASE.
PRINTS; PRO0014; FNTYPEIII.
Transferase; Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 96068901.
                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: TYPE I M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE --
TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KINASE RECEPTOR) (TCK).
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                 DOMAIN
                                                        21 LMDTKWTTSELAWVAYPDSG
                                                                          3 LLDSKTIQGELGWISYPSHG
                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
                                                                                             Similarity 45.
9; Conservative
                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                            974 AA;
                                                                                                                                                                                                    535
535
536
178
178
316
609
609
         PRELIMINARY;
                                                                                                                                                               16
974
534
555
102
102
102
315
315
623
623
734
734
758
                                                                                                                                            108263
                                                                                                      45.08;
                                                                                                                                                                                                                                                                                                           Glycoprotein;
POTENTIAL.
                                                        40
                                                                          22
                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RENAUD C
                                                                                            4
                                                                                            Score 57; DB Pred. No. 1.1; 4; Mismatches
                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY,
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL) IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                               FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                   CYS-RICH
                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                 EPHRIN TYPE-B RECEPTOR
                                                                                                                                                                                                                                                                                                                  kinase; ATP-binding; Phosphorylation; oprotein; Signal; Immunoglobulin domai
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I MEMBRANE PROTEIN
SED IN THE EMBRYO I
                                                                                                                                            BD419F6D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.S., SHEA L.J.,
tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF THE
         1055 AA
                                                                                                               DB 13; Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPHRIN-B FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IN PRE-SOMITIC
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OVARY. LOWER LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SARGENT T. subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP + PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphibia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       f.D.;
Y expressed
                                                                                           0,
                                                                                                                                                                                                                                                                                                                    domain.
                                                                                           Gaps
                                                                                           0
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O43569;
C 043569;
C 043569;
C 043569;
T 01-JUN-1998 (TIEMBLIEL. 06, Last sequence updat of the control of the c
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Best Local S
Matches 10
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HSSP; P00523; 2PTK.
HSSP; P00523; 2PTK.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PFAM; PF01404; EPH_lbd; 1.
PFAM; PF01404; fn3; 2.
PFAM; PF00069; Pkinase; 1.
PFAM; PF000536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE: 961546/3.

MEDLINE: 961546/3.

IKEGAKI N., TANG X.X., LIU X.G., DIEGER, SULMAN E.P., BRODEUR G.M., PLEASURE D.E.;

SULMAN E.P., BRODEUR G.M., PLEASURE D.E.;

"MOLECULAR Characterization and chromosomal localization "MOLECULAR CHARACTERIZATION and Chromosomal localization generally a developmentally regulated human protein-tyrosigene of the EPH family.";

Hum. Mol. Genet. 4:2033-2045(1995).
                                                                                                                                                                                                                                                                                      STEIN E.,
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

TANG X.X., PLEASURE D.E., IN
Submitted (SEP-1997) to the
EMBL; AF025304; AAB94602.1;
HSSP; P00523; 2PTK.
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01-JUN-1998
                                                                                                                                                             EMBL;
HSSP;
PFAM;
                                                                                                                                                                                                                                                                                                             STEIN
                                                                                                                                                                                                                                                      EMBL;
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PRINTS; PRO0109; TYRKINASE.
TYROSINe-protein kinase.
SEQUENCE 1055 AA; 117492
                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN-TYROSINE
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IN E., SCHÖECKLMANN H.O., D
titted (DEC-1997) to the EM;
FRO37333; AAB94627.1; -.,
AF037334; AAB94628.1; -.,
PO06631; ARCK.
PF000631; ARCK.
PF00069; pkinase; 2.
PF00069; pkinase; 2.
PF01404; EPH_LDd; 1.
PF01404; EPH_LDd; 1.
PF01404; FROYPEIII.
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Chordata; Craniata; Vej
Catarrhini; Hominidae;
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50.0%;
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. 06, Last sequence upo
. 12, Last annotation u
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ne EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB
Pred. No. 1.7;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                   DANIEL
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                                                                                                                                                                                                                                                                                                                   T.O.;
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1.7;
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Best Local S
Matches
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907494
Q07494;
Q07494;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1999 (TrEMBLrel. 12)
1 01-NOV-1999 (TrEMBLrel. 12
                                  "Five ....;
expressed.";
Oncogene 8:1807-1813(1993).
EMBL; Z19110; CAA79526.1; -.
EMBL; Z1910; CAA79526.1; -.
D00523; ZPTK.
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                                                                                                                                                                                                               Neognathae;
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EMBL; AF037331; AADD20300.1; -.:

HSSP; P00523; 2PTK.

PROSITE; PS00107; PROTEIN_KINASE_ATP;

PROSITE; PS00109; PROTEIN_KINASE_TYR;
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EPHA
Homo sapiens (Human).
Homo sapiens (Human).
Homo sapiens (Human).
Larvota; Metazoa; Chordata; Ci
                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Neognathae; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor; Kinase.
SEQUENCE 984 A
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01-NOV-1999
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              EMBL; Z19110; CAA79526.1; --
HSSP; P00523; ZPTK
PROSITE; PS00109; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
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J. Biol. Chem. 0:
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                                                                                                                                         MEDLINE; 93288394.
SAJJADI F.G., PASC
                                                                                                                     SAJJADI F.G., PASQUALE E.B.;
"Five novel avian Eph-related
                                                                                                                                                                              TISSUE-BRAIN;
                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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9; Conserv
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                                                                                                                                                                                                                            Chordata; Craniat;
rmes; Phasianidae;
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01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB Pred. No. 2.1; 5; Mismatches
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                                                                                                                                                                                                                             Craniata; Vertebrata;
ianidae; Phasianinae; (
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                         tyrosine kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CERRETTI D.P., r, EphB1/ELK, co
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on update)
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                                                                                                                                                                                                                             : Archosauria;
Gallus.
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Best Local S
Matches 9
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PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; FA
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FA
PFAM; PF00041; fn3; 2.

PFAM; PF00069; Pkinase; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF01104; EPH_Ibd; 1.

PFAM; PF01104; EPH_Ibd; 1.
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015197;
01-JAN-1998
01-JAN-1998
01-NOV-1999
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PFAM; PFO
PFAM; PFO
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SEQUENCE
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TRANSMEM
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Primates; Catarrhini; Hominidae;
                                                                                             Glycoprotein;
SIGNAL
                                                                                                                                                                                                           DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
EMBL; D83492; BAA21560.1; -.
EMBL; AF107256; AAD03058.1; -.
                                                                                                                                                                                                                                                                        -1: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1: TISSUE SPECIFICITY: STRONG EXPRESSION IN THE BRAIN AND PANCREAS AND WEAK EXPRESSION IN OTHER TISSUES, SUCH AS THE HEART, PLACED LUNG, LIVER, SKELETAL MUSCLE AND KIDNEY.
-1: SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 97350806.
MATSUOKA H., IWATA N., ITO M., SHIMOYAMA M., NAGATA
TAKAI S., MATSUI T.;
"Expression of a kinase-defective Eph-like receptor
human brain.";
                                                                                                             PRINTS; PRO0014; FNTYPEIII.
Transferase; ATP-binding; Phosphorylation; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                   TAUDIEN S., ROSENTHAL A.;
Submitted (NOV-1998) to the
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-804 FROM
                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPH-FAMILY
                                                                                                                                                                                                                                                                                                                                         FUNCTION: KINASE-DEFECTIVE
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PF01404;
PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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8 (TremBlrel. 05, 1
9 (TremBlrel. 12, 1
RECEPTOR PROTEIN 1
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                                                                                 ; Signal;
1 16
17 1006
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EPH_1bd;
fn3; 2.
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                               OGIODUIN domain.
BY SIMILARITY.
BY SIMILARITY RECEPTOR PROTEIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
**C-**TYPE DOMAIN.
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Last annotation update)
PRECURSOR (EC 2.7.1.112)
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                  IG-LIKE C
POLY-SER
CYS-RICH.
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Pred.
FIBRONECTIN POLY-GLY.
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         TYPE-III
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EMBERS OF T
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Best Local S
Matches
                                                                                                                                                                                                  MGD; MGI:108444; Cekl.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; FF
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FF
PRAM; PF00041; fn3; 2.

PFAM; PF00069; pkinase; 1.

PFAM; PF01040; EPH_lbd; 1.

PRINTS; PR00014; FNTYPEIII.
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CARBOHYD
SEQUENCE
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TRANSMEM
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                                                                                                                                                Transferase; ATP-binding; Phosphorylation; Re Glycoprotein; Signal; Immunoglobulin domain; SIGNAL 1 32 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                      EMBRYONIC STEM CELLS.

1. SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

1. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN

1. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

EMBL; L77867; AAB51430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96358627.
GURNIAK C.B., BERG L.J.;
"A new member of the Eph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UU-1997 (TremBLrel. 04, Created)
01-UU-1997 (TremBLrel. 04, Last sequence update)
01-NOV-1999 (TremBLrel. 12, Last annotation update)
EPH/ELK RECEPTOR-LIKE PROTEIN PRECURSOR (MEP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine kinase activity.
Oncogene 13:777-786(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEKL OR MEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 008644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                008644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: HIGH LEVEL IN THYMUS, AND LEVELS OF EXPRESSION IN KIDNEY, LUNG, LIVER, B MUSCLE, SPLEEN FROM 2 WEEK OLD AND ADULT MICE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOFORMS ARE SECRETED.
ALTERNATIVE PRODUCTS: AT LEAST
ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMILY
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9; Conserv
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PROTEIN KINASE-LIKE.
POLY-PRO.
ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred.
CYS-RICH.
FIBRONECTIN TYPE-III.
                                                       CYTOPLASMIC (POTENTIAL) IG-LIKE C2-TYPE DOMAIN.
                                                                                           EXTRACELLULAR (POTENTIAL) POTENTIAL.
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                                                                                                                               EPH/ELK RECEPTOR-LIKE PROTEIN.
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                                                                                                                                                                                                                                                                                               FALSE_NEG.
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, BONE MARROW, SKE
CE, HEART, TESTES
                                                                                                                                                                                                                                                                                                                                                                                                                                            IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARE
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01-JUN-1998
01-NOV-1998
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01-NOV-1996
01-NOV-1996
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053825;
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ROBISON K.;
Submitted (SEP-1994) to the EM
Submitted (SEP-1994) to the EM
EMBL; U15182; AAA62976.1; ".
EMBL; U5182; AAA62976.1; ".
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NP_BIND
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DOMAIN
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Bacteria; Firmicutes; Actinobacteria; Actinobacterida; Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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                                               HAMLIN N.,
                                                                STRAIN-H37RV;
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                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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Submitted (DEC-1995) to the Empl., 269662; CAA93506.1; -.
EMBL; 269662; CAA93506.1; OINED.
EMBL; 268214; CAA92448.1; -.
EMBL; 269662; CAA92448.1; JOINED.
R EMBL; 269662; CAA92448.1; JOINED.
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Q17901; Q20887;
01-NOV-1996 (TTEMBLTel. 0
01-NOV-1998 (TTEMBLTEL. 0
01-JAN-1999 (TTEMBLTEL. 0
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 94150718.
MILSON R., AINSCOUGH I
BONFIELD J., BURTON J.
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MATTHEWS
                                                                                                                                                                                   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FUTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINGRE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.;
"2 MATSON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLE S.T., PARKHILL J., Submitted (FEB-1997) to [3]
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C10C5.6A.
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EMBL; AL022004; CAA17617.1; -.
Hypothetical protein.
SEQUENCE 368 AA; 39447 MW;
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PHILIPP W.J., POULET
BALASUBRAMANIAN V., F
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Rhabditidae; Peloderinae; C
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2; Mismatches
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             PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_U_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_U_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_U_2; 1.

PROSITE; PS00186; EGF_2; UNKNOWN_1.

PROSITE; PS00186; EGF_2; UNKNOWN_1.

PFPAM; PF00046; PKinase; 1.

PFAM; PF000556; SAM; 1.
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CCHICK STANDARD; PRT; 983 AA.
P29318;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETKI) (CEK4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
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"Identification of a new eph-related receptor tyrosine kinase gene
from mouse and chicken that is developmentally regulated and encode;
at least two forms of the receptor.";

New Biol. 3:769-778(1991).

"I FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
EPHRIN-A2, -A3, -A4 AND -A5.

"I CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSIME PHOSPHATE.

"I SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

"I SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPHA3 OR ETK1 OR CEK4.
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M68514; AAA48666.1;
PIR; B45583; B45583.
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 92031278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATAL DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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                                                          PF01404; EPH_1bd; 1.
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WAPP_COCIM
WAPP_COCIM
FIXN_AZOCA
EPHA_MOUSE
ETAM_ECOLI
DCAM_ECIDO
COA2_HUMAN
FRDD_MYCTU
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P47808
P47808
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P43167
P98056
P54761
P37669
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                    Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilk Welch K., Loudovaris M., Rockman S., Busmanis I.; "Isolation and characterization of a novel receptor-type protein tyrosine kinase (hek) from a human pre-B cell line."; J. Biol. Chem. 267:3262-3267(1992).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
                                                                                                                                                                                                                                                               Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.; "Molecular cloning of HEK, the gene encoding a receptor kinase expressed by human lymphoid tumor cell lines."; Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
                                                                                                                                                                                                                                                                                                                                                                                                    EPA3_HUMAN STANDARD; PRT; 9
EP3320;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC
KINASE RECEPTOR ETKL) (HEK).
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 92179233.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Ci
Eutheria; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                        PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: RESTRICTED TO LYMPHOID TUMOR CELL LIN
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                              FUNCTION.

CATALYTIC ACTIVITY: ATP + A PROTEIN
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EPHRIN TYPE-A RECEPTOR 3.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYS-RICH.
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Pred. No. le-
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7; E8895F0BDF77651E CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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i; Hominidae;
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2 2.7.1.112) (TYROSINE-PROTEIN
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PRT; 983 AA.

P29319;

01-DEC-1992 (Rel. 24, Created)

01-DEC-1992 (Rel. 24, Last sequence update)

101-NOV-1997 (Rel. 35, Last annotation update)

101-NOV-1997 (Rel. 35, Last annotation update)

EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.1)

KINASE RECEPTOR ETK1) (MEK4).

EPHA3 OR ETK1 OR MEK4 OR TYRO4.
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PRINTS; PRO0109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGE_2; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PEAM; PF00041; fn3; 2.

PEAM; PF000536; SAM; 1.

PEAM; PF000536; SAM; 1.

PEAM; PF01404; EPH_1bd; 1.

Transferase; Tyrosine-protein kinase; ATP-bir
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MIM; 17961:
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                  SEQUENCE FROM N.A.
STRAIN-ICR X SWISS
MEDLINE; 92031278.
                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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22; Conser
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an email to license@isb-sib.ch)
F.G.,
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                                       WEBSTER;
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Sciurognathi; Muridae;
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  E.B.,
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Glycoprotein; Signal.
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CYTOPLASMIC (POTENTIAL
CYS-RICH,
FIBRONECTIN TYPE-III,
FIBRONECTIN TYPE-III.
                                       TISSUE-EMBRYO;
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  Subramani S.;
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Pred. No. 1e-10;
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-> L (IN CAA01906).
B8D900FA80FF5121 CRC64;
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: 2.7.1.112)
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                                                                                                Vertebrata;
ae; Murinae;
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VNLLDSKTIQGELGWISYPSHG

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Query Match
Best Local
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PRINTS; PRO0109; TYRKINASE.ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PRAM; PF00064; fn3; 2.

PFAM; PF00065; PKinase; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF00536; SAM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M68513; AAA39521.1; -.
EMBL; M68515; AAA39522.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor.";

New Biol. 3:769-778(1991).

-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PRO0014; FNTY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A45583
                   Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPHRIN-A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -

PROTEIN TYROSINE PHOSENER -

PROTEIN TYROSINE PHOSENER -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE
                 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P16109;
l Similarity
22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                    Conservative
                                                                                                                                                                                                                                                                                                                 Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A45583.
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                                                                                                                                                 Ä
                                                                       100.0%;
                                                                                                                                                   109955
                                                                                         .08;
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BY SIMILARITY
                                                                                                                                               MW;
                                                                                                                                                                            BY SIMILARITY. AUTO-) (
PHOSPHORYLATION (AUTO-) (
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                 22
                                                    0;
                                                                                                                                                                                                                                                                                               ATP
ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                   MISSING
                                                                                                                                                                                                                                                                                                                                                                       FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase; ATP-binding; Phosphorylation;
oprotein; Signal; Alternative splicing
                                                                         Score 119;
Pred. No. 1
                                                                                                                                               BE44A6655D8107A2 CRC64;
                                                      Mismatches
                                                                                                                                                                                                                                                                                                               (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                        KINASE.
                                                                     1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                         DB 1;
                                                      0,
                                                                                       Length 983;
                                                      Indels
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                                                    0;
                                                    Gaps
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EPA3_RAT
008680;
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
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DOMAIN
                                                                                                                                                                                       PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
Transferase; Tyrosine-protein kinase; ATP-binding;
                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "IL-1 beta alters the expression of the receptor tyrosine kinase gene r-EphA3 in neonatal rat cardiomyocytes.";
Am. J. Physiol. 274:H331-H341(1998).
-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR REK4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAT
                                                                                                                                                                      Receptor;
SIGNAL
                                                                                                                                                                                                                                                           EMBL; U69278; AACO6273.1; -. HSSP; P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                       entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                 DOMAIN
                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 98120505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                           send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y.Y., McTiernan C.F., Feldman A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA
DOMAIN. BELONGS TO THE EMBRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                 ITE; PSU0791; RECEPTOR TYRKIN, IITE; PS01186; EGF_2; UNKNOWN_1. PF00041; fi3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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RECEPTOR_TYR_KIN_V_2; 1.
 984
541
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432
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883
636
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                                                                                                                                                                      Glycoprotein;
BY SIMILA
POTENTIAL.
                                                         ATP
                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL)
CYS-RICH.
                                                                                                                                            BY SIMILARITY.
EPHRIN TYPE-A RECEPTOR 3.
EXTRACELLULAR (POTENTIAL)
                                                                                       FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                      POTENTIAL.
                                                                             PROTEIN
                                 PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                            SIMILARITY
                                                       SIMILARITY).
SIMILARITY).
                                                                            KINASE.
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                                                                                                                                                                                 Signal.
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                                  (BY SIMILARITY)
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EPA5_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
                                                                    PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PSO0107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.

PROSITE; PS00719; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.

PFAM; PF00060; Pkinase; 1.

PFAM; PF00053; SAM; 1.

PFAM; PF011404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFA5_CHICK
P54755;
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CARBOHYD
SEQUENCE
       Transferase;
Receptor; Tra
SIGNAL
                                                                                                                                                                                                                                                                                                                                             EMBL; UC
HSSP; PC
PRINTS;
                                                                                                                                                                                                                                                                                                                                                                      EMBL; U03910;
EMBL; U03910;
EMBL; U03910;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-197 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a complete Cek7 receptor protein tyrosine kinase coding sequence and cDNAs of alternatively spliced transcripts."; Gene 148:219-226(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPHA5 OR CEK7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE BHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNLLDSKTIQGELGWISYPSHG
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22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95047429.
se: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
Transmembrane; Glycoprotein; Signal; Alternative splicing
1 31 POTENTIAL.
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493
984
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                                                                                                                                                                                                                                                                                                                                                                   AAB60613.1; -.
AAB60614.1; -.
AAB60612.1; -.
2PTK.
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493
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POTENTIAL.
s; F170C49312F7A0AB
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Pred. No. 1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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Best Local S
Matches 15
       EMBL; U07357;
HSSP; P00523;
MGD; MGI:99654
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ACT_SITE
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    Zhou R., Copeland T.D., Kromer L.F., Schulz N.T.;
"Isolation and characterization of Bsk, a growth factor receptor-like tyrosine kinase associated with the limbic system.";
J. Neurosci. Res. 37:129-143(1994).
1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.
KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                        EPHA5 OR EHK1 OR CEK7 OR BSK.
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nes 15; Conservative
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                                                                                                                                        PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: BRAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CAT
SOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
        MGI:99654; EPHAS
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Rodentia; Sciurognathi; Muridae; Murinae;
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                               AAA17038.1;
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                                                                                                                                                                                                                                                                                                                                                                                                              annotation update)
ECURSOR (EC 2.7.1.112) (TYROSINE-PRO
HOMOLOGY KINASE-1) (BRAIN-SPECIFIC
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POTENTIAL.

MISSING (IN ISOFORM 2).

SCCDHGCGWASSLRAVAYPSLIW -> R (IN ISOFORM 1).

1 AND ISOFORM 2).
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POTENTIAL.
POTENTIAL.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR
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1.1e-06;
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Mus.
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PR00014; FNTYPEIII

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PFAM; PF00069; PKinase; 1.
PFAM; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O09127;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 8 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN EPHRIN TYPE-A RECEPTOR 8 PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                   kinases, can be activated by three (
Oncogene 14:533-542(1997).
-I- FUNCTION: RECEPTOR
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CARBOHYD
SEQUENCE
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SIGNAL
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park
"The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 97178845.
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PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

PROTEIN TYROSINE PROSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                        DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00536; SAM; 1.
PF01404; EPH_lbd; 1.
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PS00790;
                                    and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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1 26 BY SIMILA
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97115 MW;
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RECEPTOR_TYR_KIN_V_2; 1.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine protein family ligands.";
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                                                                                                                                                                   restrictions
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Best Local S
Matches 14
                                    Basu R., Welcher A.A.; "unce H.T., Linc "cDNA cloning and tissue distribution protein-tyrosine kinases."; Oncogene 10:897-905(1995).
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BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
                                                                                                                                                                                               01-OCT 1996 (Rel. 34, Created)
01-OCT 1996 (Rel. 34, Last sequence update)
10-UCT-1998 (Rel. 34, Last sequence update)
15-UU-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN-
KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-
TYROSINE KINASE HEK7).
EPHA5 OR EHKI OR HEK7.
HOMO sapiens (Human).
EPHA5 OR EHKI OR HEK7.
                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                     MEDLINE; 95206782.
Fox G.M., Holst P.
                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                          P54756;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
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PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00790; RECEPTO PROSITE; PS00791; RECEPTO PROSITE; PS01186; EGF_2; PFAM; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:109378; EPHA8.
PRINTS; PRO0014; FNTYPEIII.
PRINTS; PRO0109; TYRKINASE.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
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                                                                                                                    SEQUENCE OF 25-1037
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                  Miescher
                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                         Eutheria;
                                                                                                                                                            "ISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iransferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                    31 VNLLDTSTIHGDWGWLTYPAHG
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                               1 VNLLDSKTIQGELGWISYPSHG
       EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN
PROTEIN TYROSINE PHOSPHATE.
                            runction: RECEPTOR FOR MEMBERS OF
                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                    HUMAN
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PF00536; SAM; 1.
PF01404; EPH_lbd; 1.
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                                                                                                                                                                                         Primates;
                                                                                        Holst P.L.,
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563
640
759
792
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LOCATION: TYPE I MEMBRANE PROTEIN
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541
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RECEPTOR_TYR_KIN_V_2;
                                                                                                                    FROM
                                                                                                                                                                                        Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                   74.8%;
63.6%;
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                                                                                                                                     the EMBL/GenBank/DDBJ databases
                                                                                                                    N.A.
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POTENTIAL
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Pred.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                       Craniata; Vertebrata;
i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                  of five
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4.7e-06;
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                 TYROSINE
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                                     EPHRIN-A
                                                                                     R.A., Janssen
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                                                                  human
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                  ADP
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                                                                  EPH-like receptor
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EMBL;
HSSP;
              EPA5_RAT STANDARD; PRT; 1005 AA. p54757; P5475
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CARBOHYD
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TRANSMEM
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SIGNAL
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PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
PROSITE; PS00101; PROTEIN KINASE_DON;
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
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PRINTS; PR00109
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                                                                                                                                                                  RAT
    EPHA5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED E ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE N SYSTEM.
SYSTEM.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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1; PF00069; pkinase; 1.
1; PF00536; SAM; 1.
1; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                         VNLLDSKTIQGELGWISYPSHG
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L36644; AAA74245.1;
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    EKH1
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    OR.
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63.
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89 89
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POTENTIAL
                       HOMOLOGY KINASE-1)
                                                                                                                                                                                                                                                  82
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Pred. No. 4.9e
6; Mismatches
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MW; FC2C46C959AFB699 CRC64;
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BY SIMILARITY.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase; ATP-binding; Phosphorylation;
oprotein; Signal; Alternative splicing
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                                                                                                                                                                                                                                                                                                                 DB 1,
4.9e-06;
2;
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                                          .112)
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                                          (TYROSINE-PROTEIN
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    PRINTS; PRO0014; ENTYPEIII.

PRINTS; PRO0109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOW; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01786; EGF_2; UNKNOWN_1.

PFAM; PF00069; Pkinase; 1.
                                                                                CARBOHYD
CARBOHYD
CARBOHYD
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                                        CARBOHYD
CARBOHYD
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                      Transferase;
                                                                                                                                                                                                                                                                                                                                                                                             PFAM;
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Transmembrane;

Glycoprotein; POTENTIAL

kinase; ATP-binding; Phospho: oprotein; Signal; Alternative

Phosphorylation;

EPHRIN TYPE-A

RECEPTOR

EXTRACELLULAR (POTENTIAL)

Tyrosine-protein pkinase; 1. EPH_lbd; 1.

576 577 597 709 709 802 802 4425 100 100

POTENTIAL.
POTENTIAL.
GRRRTQGRGGG -> [
SPLICED FORMS).

DADGPRAQASWCHARR (IN

POTENTIAL.
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POTENTIAL. BY SIMILARITY.

1005 575 596 1005 938 691 709 802 266 266 425 438 438

ATP

(BY SIMILARITY). (BY SIMILARITY).

CYTOPLASMIC (POTENTIAL).

PROTEIN KINASE POTENTIAL.

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Elk-like receptor tyrosine kinase in brain.";

Neuroscience 63:163-178(1994).

-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A

-I- CAPALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -

-I- CAPALYTIC TYROSINE PHOSPHATE.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE
                                                                                                                                                                                                                 entitles requires a local property of the second of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lassmann H., Steck A.J.;
"Expression and developmental regulation of Ehk-1, "it receptor tyrosine kinase in brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maisonpierre P.C., Barrezueta N.X., Yancopoulos G.D.; "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Eutheria; Rodentia; Sciu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; MEDLINE; 95206467.
                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taylor V., Pfarr S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS
X78689; CAA55357.1;
P00523; 2PTK.
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miescher G.C., Honegger P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RS OF THE EPHRIN-A FAMILY.
                                                                                                                                                                                                           (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARE PRODUCED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal
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SEQUENCE
                                                                     This SWI
                                                                                                                                                                                                                                                                                                                                          MEDLINE;
Ohta K.,
   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                               Ando
                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phasi
                                                                                                                                                                                                                                                                                                                                                                                                                                           EPA4_CHICK STANDARD; PRT; 986 AA. 007496; Q90772; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8).
                                                                                                                                                                                      Oncogene 8:1807-1813(1993).
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE-SPINAL CORD;
                                                                                                                                                                                                             expressed."
                                                                                                                                                                                                                                   MEDLINE; 93288
Sajjadi F.G.,
                                                                                                                                                                                                                                                                     SEQUENCE OF 138-986
                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHA4 OR CEK8.
                                                                                                                                                                                                                       "Five novel avian
                                                                                                                                                                                                                                                            TISSUE-EMBRYO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VNLLDSKTIQGELGWISYPSHG
                                                                                                 FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CADOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                      receptor tyrosine kinase, pes of motoneurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNLLDSRTVLGDLGWIAFPKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
14; Conserv
                                                                                                                                                                                                                                                                                                                              Tanaka H.;
                                                                                                                                                                                                                                             93288394.
                                                                                                                                                                                                                                                                                                                                        Nakamura M., Hirokawa
                                                                                                                                                                                                                                                                                                                                                      96404128
                                                                                                                                                                                                                                                                                          54:59-69(1996).
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vian Eph-related
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KCNSHAGVCEECGGHVRYLPQQIGLKNTSVMADPLAHTNY
TFELEAVNGVSDLSPGTRQYVSVNVTTNQAA -> T (IN
SPLICED FORMS).

SGSCCECGCGRASSLCAVAHPSLIW -> R (IN
SPLICED FORMS).

D -> E (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
T -> I (IN REF. 2).
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Archosauria; Aves;
ianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                       tyrosine
                                                                                                                                                                                                                                                                                                                                        ×;
                                                                                                                                                                                                                                                                                                      Cek8, is transiently expressed spinal cord during development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                        Tanaka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
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9.6e-06;
2;
                                                                                                                                                                                                                       kinases
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                                                                   EMBL
                                                                                                                 CATALYTIC
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AND A-3.
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                                                                            collaboration
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                                                                   outstation
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RESULT
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Best Local S
Matches 14
 protein-tyrosine kinases.";
Oncogene 10:897-905(1995).
-i- EUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A1, -A4 AND -A5. BINDS MORE POC.
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TY PROTEIN TYROSINE PHOSPHATE.
-i- SUBCETITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D38174; BAA07373.1; -.

EMBL; Z19059; CAA73509.1; -.

HSSP; P00523; ZPTK.

HSSP; P00523; ZPTK.

HSSP; P00014; FNUYPEIII.

PRINTS; PR00104; FNOTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.

PFAM; PF00069; pkinase; 1.

PFAM; PF00069; pkinase; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF001404; EGF_1016; PFAM; PF00536; SAM; 1.

PFAM; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Cr
01-OCT-1996 (Rel. 34, Le
15-JUL-1998 (Rel. 36, Le
EPHRIN TYPE-A RECEPTOR 4
KINASE RECEPTOR SEK) (RE
EPHA4 OR SEK OR HEK8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
NP_BIND
BINDBIND
BINDT

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _HUMAN
                                                                                                                               Basu R., Welcher A.A.;
"cDNA cloning and tissue
                                                                                                                                                                   Fox G.M.,
                                                                                                                                                                     TISSUE-BRAIN;
MEDLINE; 95206782.
Fox G.M., Holst P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEN
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                  Eutheria;
                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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| ||||::::||||||: |
31 VTLLDSRSVQGELGWIASPLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 63.1
14; Conservative
                                                                                                                                                                                                                                FROM
                                                                                                                                                                                                                                                                    ; Metazoa;
Primates;
                                                                                                                                                                                                                                                                                                (Rel. 34, Createu,
(Rel. 34, Last sequence update)
3 (Rel. 36, Last annotation update)
5-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN TYROSINE KINASE HEK8).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 R
487 S
109482 MW;
                                                                                                                                                                                                                                                                  Chordata; C:
Catarrhini;
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                                                                                                                                                                       Chute H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 48;
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POTENTIAL
TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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POTENTIAL.
POTENTIAL.
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FIBRONECTIN TYPE-III
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                  Craniata; Vertebrata; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> G (IN REF. 2).
-> T (IN REF. 2).
BD88C2A5BD84OAOF CRC64;
                                                                                                                                                                     Lindberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                               986
                                 THE EPHRIN-A FAMILY. BINDS TO E POORLY TO EPHRIN-A2 AND A-3. IN TYROSINE = ADP +
                                                                                                                                   of five
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.00017;
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                                                                                                                                                                     R.A.,
                                                                                                                                   human
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                                                                                                                                                                     Janssen
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                                                                                                                               EPH-like receptor
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SIMILARITY).
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RESULT 12
EPA4_MOUSE
ID EPA4_M
AC Q03137
DT 01-OCT
DT 01-NOV
DE EPHA4
DE KINASE
GN MUS MUS
OC ENTHER
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RX MEDLI1
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Matches 14
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00701; PROTEIN_KINASE_DOM; 1.

PROSITE; PS007790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PFAM; PF00041; fn3; 2.

PFAM; PF00040; PK10ase; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF01404; EPH_1bd; 1.

Transferase; Tyrosine-protein_kinase; ATP-1
                                                              EPHA4 OR SEK.

Mus musculus (Mouse).

Eukaryota; Metazoa; C

Eutheria; Rodentia; S
                                                                                                                       EPA4_MOUSE STANDARD; PRT; 986 AA. 003137; 01-OCT-1994 (Rel. 30, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) KINASE RECEPTOR SEK) (MPK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a clear the Ewiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
   SEQUENCE FROM N.A.
STRAIN-C57BL; TISSUE-EMBRYONIC
MEDLINE; 93096484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor;
                                                                                                                                                                                                                                                                                                          31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN. BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                         VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                        VTLLDSRSVQGELGWIASPLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L36645;
                                                                                                                                                                                                                                                                                                                                                                     Similarity 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621
627
653
746
779
235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548
570
436
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TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Ve. Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                      63
63
                                                                                                                                                                                                                                                                                                                                                                                                                                                     109859
                                                                                                                                                                                                                                                                                                                                                                                      .68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FIBRONECTIN TYPE III-LIKE DOMAINS.
PROTEIN-TYROSINE KINASES IN THE CATALYTIC
HE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASE.
AIP (BY SIMILARITY).
AIP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
OC39C1152EDDD46F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹.
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                                                                                                                                                                                                                                                                                                                                                                     4:
                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                      Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPHRIN TYPE-A RECEPTOR 4. EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.0
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal
                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                Vertebrata;
se; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                       .00017
                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                 Length 986;
                                                                                                                                            (TYROSINE-PROTEIN
                                                              Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n 0
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PRINTS; PRO0104; FNYPEIII.

PRINTS; PRO0109; TYRKINASE.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PEAM; PF00041; fn3; 2.

PFAM; PF00041; fn3; 2.

PFAM; PF000516; SAM; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF01404; EPH_Lbd; 1.

Transferase; Tyrosine-protein kinase; ATP-1

Transferase; Tyrosine-protein kinase; ATP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";
Oncogene 7:2499-2506(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X65138;
EMBL; X57241;
EMBL; S57168;
HSSP; P00523;
                    ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                         DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                               Receptor;
SIGNAL
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gilardi-Hebenstreit P., Ni
Chestier A., Wilkinson D.G
Oncogene 8:1103-1103(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                           TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN ALTERNATIVE PRODUCTS: A SHORTER FORM WITH A DI AMINO ACIDS ALTERLING THE CATALYTIC SITE MAY BI ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-MAY PLAY A ROLE IN A SIGNAL TRANSDUCTION PROCESS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LI SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: HIGHEST LEVELS IN THE HEART, LUNG AND KIDNEY. IT IN THE EMBRYONIC BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HINDBRAIN PATTERN FORMATION.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:98277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93205393
                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CAA46268.1; -.; CAA40517.1; -.; AAB25836.1; -.; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPHA4.
  109801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nieto
                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
  ¥.
                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (BY
FIBRONECTIN TYPE-III (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O M.A., Frain M., Charnay P.;
                                                           PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                    PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                    MISSING
                                         POTENTIAL
                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                             EPHRIN TYPE-A
EXTRACELLULAR
                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
D16AD8B85668C80E CRC64;
                  (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Phosphorylation; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S IN THE BRAIN, IS SEGMENTALLY
                                                                                                                                                                                                                                                                                                                           RECEPTOR 4. (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 III-LIKE
INASES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattei M.-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAINS.
THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOWER LEVELS
EXPRESSED
                                                                                                                                                                                                                                         SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN -
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RESULT
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                                                        Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00107; E
PROSITE; PS00109; E
PROSITE; PS50011; E
PROSITE; PS00790; E
PROSITE; PS00791; E
PROSITE; PS01186; E
                                                                                                                                                         NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinase family with distinctive structures and neuronal expression.";
Oncogene 8:3277-3288(1993).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, C
01-OCT-1996 (Rel. 34, I
01-NOV-1997 (Rel. 35, I
EPHRIN TYPE-A RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maisonpierre P.C., Barrezueta N.X., Yancopoulos G.D.; "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94067777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINASE RECEPTOR EHK-2)
EPHA6 OR EHK2 OR EHK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31
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1 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTLLDSRSVQGELGWIASPLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00069; pkinase; PF01404; EPH_lbd;
                                                          l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 63.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR0001
                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                     409
948
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2PTK
                                                                                                                                                           Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PROTEIN_KINASE_ATP; 1.
; PROTEIN_KINASE_TYR; 1.
; PROTEIN_KINASE_DOM; 1.
; PROTEIN_KINASE_DOM; 1.
); RECEPTOR_TYR_KIN_V_1; 1
; RECEPTOR_TYR_KIN_V_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34, Last sequence update)
35, Last annotation update)
EPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
HK-2) (EPH HOMOLOGY KINASE-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF_2; UNKNOWN_J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                             106235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.4%;
                                                                          61.3%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
POTENTIAL.
                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 79; DB . Pred. No. 0.007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
                  22
                                                        4;
                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                         POTENTIAL.

1; A47DC78EDB2DEF30 CRC64;
                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                 POTENTIAL.
                                                        Mismatches
                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             948
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Phosphorylation;
                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                               DB 1;
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                                                                            0014;
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Rattus.
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RESULT 14
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ID EPA6_MOUSE
AC Q62413;
DT 01-NOV-1997
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS000790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS000790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS000791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.
                                                              DOMAIN
TRANSMEM
DOMAIN
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CARBOHYD
                                                                                                                                                                                                                                                      Receptor;
SIGNAL
CHAIN
                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                               PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee A.M., Navaratnam D., Ichimiya S., Greene M.I., Davis J.G.;
"Cloning of m-ehk2 from the murine inner ear, an eph family recep
tyrosine kinase expressed in the developing and adult cochlea.";
DNA cell Biol. 15:817-825(1996).

-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U58332; AAB53836.1; -. HSSP; P00523; 2PTK. MGD; MGI:108034; EPHA6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHA6 OR EHK2 OR EHK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, I
01-NOV-1997 (Rel. 35, I
EPHRIN TYPE-A RECEPTOR
KINASE RECEPTOR EHK-2)
SEQUENCE
                                                                                                                                                                                                                                                                                                                              Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                   Transmembrane;
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116137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
R 6 PRECURSOR (EC 2.7.1.112)
) (EPH HOMOLOGY KINASE-2).
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POTENTIAL.
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                                                                                                            PROTEIN KINASE.
ATP (BY SIMILAR
ATP (BY SIMILAR
                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                     POTENTIAL
                                             POTENTIAL
                                                                 BY SIMILARITY POTENTIAL.
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EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                       kinase; ATP-binding; Phosphorylation;
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                                                                                                                                                                                                                           RECEPTOR 6. (POTENTIAL)
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n eph family receptor
adult cochlea.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TYROSINE-PROTEIN
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Mus.
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RESULT
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                                                                                                                   R PRINTS; PRO0014; FNTYPEIII.

R PRINTS; PRO0109; TYRKINASE_ATP; 1.

R PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

R PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS01186; EGF_2; UNKNOWN_1.

PFAM; PF00041; fn3; 2.

R PFAM; PF00041; fn3; 2.

R PFAM; PF000536; PAINASE; 1.

R PFAM; PF00059; PAINASE; 1.

R PFAM; PF01404; EPH_lbd; 1.

R PFAM; PF01404; EPH_lbd; 1.

R PFAM; PF01404; EPH_lbd; 1.
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPA7_HUMAN STANDARD; PRT; 998 AA. Q15375; Q15375; Q1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 15-JUI-1998 (Rel. 36, Last annotation update) EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3) (RECEPTOR PROTEIN-TYROSINE KINASE HEK11).
   TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                              Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                       EMBL; L36642; AAA74243.1;
HSSP; P00523; 2PTK.
MIM; 602190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "CDNA cloning and tissue distribution of five human EPH-like receptor protein tyrosine kinases.";

Oncogene 10:897-905(1995).

-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.

-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fox G.M., Holst P.L., Basu R., Welcher A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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| | |||: |: |||| :|| :|
34 VVLLDTTTVMGELGWKTYPLNG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
   ; Transmembrane; (
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59.1%;
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                                                                                              Glycoprotein;
POTENTIAL.
EPHRIN TYPE-A RECEPTOR 7.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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ATP (BY SIMILARITY).
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                              POTENTIAL.
                                                       479B9CA0D2BB06EB CRC64;
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Search completed: May 9, 2000, 22:32:08
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RESULT 2 A38224 C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 31-Dec-1993 #sequence_rev C; Accession: A38224; B38224 R; Wicks, I.P.; Wilkinson, D.; Sal- Proc. Natl. Acad. Sci. U.S.A. 89; A; Title: Molecular cloning of HEK A; Reference number: A38224; MUID: A; Accession: A38224 A; Molecule type: mRNA	Query Match Best Local Similarity 100.0%; Matches 22; Conservative 0 OY 1 VNLLDSKTIQGELGWISYPSHG 2	AJ> GB:M68514; NI GB:M68514; NI racted from N in-tyrosine N ophosphorylat optein kinase otein kinase	G: Pasquale, E 769-778, 1991 itification of a number: A45583; B45583	RESULT 1 B45583 receptor tyrosine kinase Cek4 - chi C;Species: Gallus gallus (chicken) C;Date: 22-Apr-1993 #sequence_revis C:Accession: B45883		31 53 44.5 976 2 32 52 43.7 1006 2 33 49 40.3 1763 2 34 48 40.3 1763 2 35 47 39.5 967 1 37 47 39.5 967 1 38 46 38.7 453 2 40 46 38.7 746 2 41 45 37.8 619 2 42 45 37.8 619 2 43 45 37.8 619 2 44 45 37.8 1576 1 45 37.8 1576 1
2.7.1.112) hek precursor - human n) ce_revision 31-Dec-1993 #text_change ce_rsalvaris, E.; Boyd, A.W. 89, 1611-1615, 1992 of HEK, the gene encoding a receptor MUID:92179233	Score 119; DB 2; Length Pred. No. 1.4e-10; 0; Mismatches 0; Indels 22	54809; PIDN:AAA48666. backbone (NCBIN:62405 be, receptor type eph; phosphoprotein; tran: logy <kin> binding motif</kin>	B.; Subramani, S. new eph-related receptor tyrosine MUID:92031278	chicken n) vision 18-Nov-1994 #text_change	ALIGNMENTS	A36355 A36355 C3C5526 T19180 T19184 T19184 AC55088 SYMTAT AC508678 B S2026678 B S2026678 B S2026678 C C C C C C C C C C C C C C C C C C C
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A; Molecule type: mRNA
A; Residues: 1-983 <WIC>
A; Residues: 1-983 <WIC>
A; Cross-references: GB: M83941; NID: g183931; PIDN: AAA58633.1; PID: g183932
A; Experimental source: pre-B-cell leukemia cell line LK63
A; Note: sequence extracted from NCBI backbone (NCBIP: 86627)
A; Accession: B38224
A; Molecule type: protein
A; Residues: 21-39; 810-860 <WIZ>
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C; Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas
F; 1-20/Domain: signal sequence #status predicted <SIG>

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A.Status: preliminary
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-983 <SAJ>
A.Cross references: GB.M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A.Cross references: GB.M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A.Note: sequence extracted from NCBI backbone (NCBIN:62398, NCBIP:62401)
C.Superfamily: protein tyrosine kinase, receptor type eph; fibronectin type
C.Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F;619-885/Domain: protein kinase homology <KIN>
F;627-635/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                               C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision
C;Accession: I50615; I50616; I50614
                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-1013 <SIE>
A;Cross-references: EMBL:U03910; NID:g555617;
A;Accession: I50616
                                                                                                                                                                                                                                                                                  R;Siever, D.A.; Verderame, M.F.
Gene 148, 219-226, 1994
A;Title: Identification of a complete Cek7
A;Reference number: I50614; MUID:95047429
A;Accession: I50615
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                                                                                                   A; Residues: 1-572,'R',596-1013 <SI2>
A; Cross-references: EMBL:U03910; NID:g555617;
                                                                                                                      A:Status: translated from GB/EN
A:Molecule type: mRNA
A:Residues: 1-572,'R',596-1013
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;Molecule type: mRNA
;Residues: 1-279,444-572,'R',596-1013 <SI3>
;Cross references: EMBL:U03910; NID:g555617;
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receptor protein-tyrosine kinase - human (fragment) (;Species: Homo sapiens (man) (;Date: 29-May-1998 #sequence_revision 29-May-1998 #te C;Accession: I78843 F.Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Oncogene 10, 897-905, 1995 Oncogene 10, 897-905, 1995 A;Fitle: CDNA cloning and tissue distribution of five A;Reference number: 158351; MUID:95206782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: Cek7
C; Superfamily: protein-tyrosine kinase, receptor type eph;
C; Superfamily: protein esplicing; ATP; transmembrane proteir; 649-915/Domain: protein kinase homology <KIN>F; 657-665/Region: protein kinase ATP-binding motif
F; 938-1004/Domain: SAM homology <SAM>
C;Superfamily: protein-tyrosine kinase, re F;627-893/Domain: protein kinase homology F;916-982/Domain: SAM homology <SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: protein-tyrosine kinase, receptor t; C;Keywords: ATP; transmembrane protein F;512-778/Domain: protein kinase homology <KIN>F;520-528/Region: protein kinase ATP-binding motif F;801-868/Domain: SAM homology <SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 brain-specific kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: 148967
R;Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz, N.T.
J. Neurosci. Res. 37, 129-143, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Isolation and characterization of A; Reference number: I48967; MUID: 94194581 A; Accession: I48967
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                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-991 < RES>
                                                                                                                                                                          A; Reference number: A; Accession: I78843
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A; Residues: 1-877 < RES>
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                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                         A; Gene: HEK7
                                                                                             A;Cross-references: GB:L36644; NID:g551611; PIDN:AAA74245.1;
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Best Local S
Matches 15
                                                                             Genetics:
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Best Local Similarity
Matches 14; Conserv
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37 VNLLDSRTVMGDLGWIAYPKNG
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                                                                                                                                                                                                                                                                                     #sequence_revision 29-May-1998 #text_change 18-Jun-1999
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68.2%;
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                                                                                                                                                                                                                                                H.T.; Lindberg, R.A.;
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Pred. No. 1.7e
5; Mismatches
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Pred. No. 6.26
6; Mismatches
                                     receptor
                     KIN>
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1.7e-06;
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6.2e-06;
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                                                                                             PID:g551612
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Query Match

Score

9;

DB 2;

Length 991;

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A; Molecule type: mRNA
A; Residues: 1-898 <TAY>
A; Residues: 1-898 <TAY>
A; Cross references: EMBL: X78689; NID: g531543; PIDN: CAA55357.1;
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibr
C; Keywords: ATP; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor tyrosine kinase - rat (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999 (C;Accession: S47489 R;Taylor, V.; Pfarr, S.; Miescher, G.C.; Honegger, P.; Breitschopf, H.; Lassmann, submitted to the EMBL Data Library, April 1994
                                      RESULT
S51604
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A;Note: the authors translated the codon GAC for residue 170 as Glu A;Note: the authors translated the codon GAC for residue 170 as Glu C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronect C;Keywords: ATP; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D. Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph re A;Reference number: S49015; MUID:94067777
A;Accession: S51603
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C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C:Accession: S51603
   C;Species:
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A; Residues: 1-893 <MAI>
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receptor-like tyrosine kinase
C; Species: Rattus norvegicus (
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Matches 14; Conserv
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| 68 VNLLDSRTVLGDLGWIAFPKNG
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63.6%;
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(Norway rat)
                   Ehk-1 -
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Pred. No.
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Pred.
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A; Molecule type: mRNA
A; Residues: 1-305, 'G', 359-1005 <MA2>
A; Residues: 1-305, 'G', 359-1005 <MA2>
A; Note: the authors translated the codon GAC for
C; Superfamily: protein tyrosine kinase, receptor
C; Keywords: ATP; transmembrane protein
F; 675-941/Domain: protein kinase ATP-binding moti
                R; Winning, R.S.; Sargen: Mech. Dev. 46, 219-229,
                                                     receptor tyrosine kinase - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
C:Accession: I51549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor tyrosine kinase Ehk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
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S49015
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R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos,
Oncogene 8, 3277-3288, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:S68029
A;Note: the authors translated the codon GAC for C;Superfamily: protein-tyrosine kinase, receptor C;Keywords: ATP; transmembrane protein
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A; Reference number: S4901:
A; Accession: S49015
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A; Residues: 1-981 <MAI>
   A; Title: Pagliaccio, a member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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A; Residues: 1-1005 <MAI>
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                                    Sargent, T.D.
                                                                                                                                                                                                                                                                        Conservative
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63.6%;
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A;Cross-references: EMBL:X65138; NID:g54083; PIDN:CAA46268.1; PID:g54084
R;G1lard1-Hebenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chestier, A.; W
Oncogene 7, 2499-2506, 1992
A;Title: An Eph-related receptor protein tyrosine kinase gene segmentally express
A;Reference number: 330496; MUID:93096484
A;A;Ccession: 330505
A;Molecule type: mRNA
A;Residues: 1-31,55-986 <GIL>
A;Residues: 1-31,55-986 <GIL>
A;Residues: 1-31,55-986 <GIL>
A;Cross-references: EMBL:X65138
C;Genetics:
C;Genetics:
A;Gene: Sek
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III:
C;Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotrans
F;1-15/Domain: signal sequence #status predicted <SIG-
F;16-986/Product: protein-tyrosine kinase Eph #status predicted <MAT>
F;548-569/Domain: transmembrane #status predicted <TMM>
F;619-885/Domain: protein kinase homology <KIN>
F;619-885/Domain: protein kinase ATP-binding motif
F;908-974/Domain: SAM homology <SAM>
F;235,340,408,423/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Accession: I51549
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-985 <WIN>
A;Cross-references: GB:L26099; NID:9416402; PIDN:AAA64
C;Genetics:
A;Gene: Pag
C;Superfamily: protein-tyrosine kinase, receptor type
C;Reywords: ATP; transmembrane protein
F;618-884/Domain: protein kinase homology <KIN>
F;626-634/Region: protein kinase ATP-binding motif
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   receptor protein-tyrosine kinase - C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence_revis C;Accession: 178844 R;Fox, G.M.; Holst, P.L.; Chute, H.
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                  ;Species: Homo sapiens (man)
;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
;Accession: 178844
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A;Gene: HEK11
C;Superfamily: I
C;Keywords: ATP
F;631-897/Domair
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protein kinase
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receptor protein-tyrosine kinase - human (Species: Homo sapiens (man) C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999 C:Accession: I58351 R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, Oncogene 10, 897-905, 1995 Oncogene 10, 897-905, 1995 A;Ritle: cDNA cloning and tissue distribution of five human EPH-like recept. A;Reference number: I58351; MUID:95206782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: I-948 < MAI>
A; Cross references: EMBL: 568030
A; Cross references: EMBL: 568030
C; Superfamily: protein-tyrosine kinase,
C; Keywords: ATP; transmembrane protein
F; 628-936/Domain: protein kinase homolog
F; 636-644/Region: protein kinase ATP-bin
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C;Genetics:
A;Gene: HEX8
C;Superfamily: protein-tyrosine kinase, re
F;619-885/Domain: protein kinase homology
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A; Molecule type: mRNĀ
A; Residues: 1-986 <RES>
A; Cross-references: GB:L36645; NID:g551613; PIDN:AAA74246.1;
                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-998 A;Cross-references: GB:L36642; NID:g551607; PIDN:AAA74243.1;
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A;Title: Ehk-1 and Ehk-2: two novel members of the Ep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor-like tyrosine kinase Ehk-2 - rat
C;Speckes: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change
C;Accession: S51605
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A;Title: CDNA cloning and tissue distribution of five A;Reference number: I58351; MUID:95206782
A;Accession: I78844
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                        A;Cross-references:
C;Genetics:
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A; Accession: S51605
A; Status: preliminary
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Title: Perfect score: Sequence:

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Scoring table:

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Total number

Sequence

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Post-processing: Minimum Match 0%
Listing first 45 summaries
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1: /cgn2_6/ptodata/;
2: /cgn2_6/ptodata/;
3: /cgn2_6/ptodata/;
4: /cgn2_6/ptodata/;
5: /cgn2_6/ptodata/
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length: 1000000
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/cgn2_6/ptodata/2/1aa/6_COMB.pep:*
/cgn2_6/ptodata/2/1aa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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US-08-162-809-16
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US-08-449-645a-21
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US-08-75-106-10
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US-08-645a-13
US-08-702-367a-3
US-08-449-645a-13
US-08-469-537a-10
US-08-673-789-3
US-08-469-537a-10
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Sequence 4, Appli
Sequence 10, Appl
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Sequence 13, Appl
Sequence 13, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 103, Appl
Sequence 15, Appl
Sequence 163, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 29, Appl
Sequence 101, Appl
Sequence 11, Appl
Sequence 17, Appl
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                                                                                                                          LENGTH: 982
TYPE: AMINO ACID
STRANDEDNESS: UNKNO
TOPOLOGY: UNKNOWN
US-08-673-789-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-673-789-4
                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/177,812
APPLICATION NUMBER: 08/177,812
EILING DATE: 04-JAN-1994
ATTORNEY_AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE_DOCKET NUMBER: 2026-41/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEFAX: 421792
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application Patent No. 5814479
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ZHOU, RENPING; SCHULZ,
APPLICANT: T.; KROMER, LAWRENCE,
APPLICANT: T.; KROMER, LAWRENCE,
APPLICANT: T.; KROMER, LAWRENCE,
APPLICANT: T.; KROMER, LAWRENCE,
APPLICANT: T.; KROMER, LESK RECEPTOR
TITLE OF INVENTION: TYROSINE KINA
TITLE OF INVENTION: USE IN DIAGN
TITLE OF INVENTION: WETHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
STREET: 345 PARK AVENUE
STREET: NEW YORK
COUNTRY: NEW YORK
COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION: 435
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Similarity 100.0%;
22; Conservative 0;
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5814479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BSK RECEPTOR LIKE
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PCT-US96-00419-2
US-08-673-789-6
US-08-426-226-2
US-08-449-645A-11
US-08-673-789-9
US-08-702-367A-19
PCT-US95-04681-11
US-08-702-367A-19
PCT-US95-04681-19
US-08-162-809-18
US-08-162-809-18
US-08-162-809-12
US-08-449-645A-20
US-08-702-367A-20
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Score 119; DB 2;
Pred. No. 1.7e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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                                            Length 982;
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Score

Query Match

Length

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774.88 44.88 45.11.33 44.48 45.11.33 46.44 46.33 46.44 46.33 46.44 46.33 46.44 46.33 46.44 46.33 46.44 46.33 46.44 46.33 46.44 46.43

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US-08-162-809-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: US-08-162-809-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/162,809
FILING DATE:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-LJ 9503
REFERENCE/DOCKET NUMBER: 9-LJ 9503
TELEPAN: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                Sequence 10, Applicat Patent No. 5674691 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5457048 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08162809 Patent No. 5457048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 43, CITY: San Diego
CITY: San Diego
CTATE: California
"nited St
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Wicks, Ian
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PASQUALE, ELENA B.
APPLICANT: SAJJAdi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 VNLLDSKTIQGELGWISYPSHG
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                                                                                                                                                                                                                                                                            Application US/08167919A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 119; DB 1; 100.0%; Pred. No. 1.7e-10; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/08449645A Patent No. 5981245
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
                                                                                                                                                                                                                                                                                        APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                              ADDRESSEE: Amgen Patent Operations/RBW STREET: 1840 Dehavilland Drive CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y match 100.0%; Score 119; DB 1; Local Similarity 100.0%; Pred. No. 1.7e-10; pes 22; Conservative 0: Miamatana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                               COUNTRY: UZIP: 91320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 18-AP
CLASSIFICATION: 435
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IBM PC compatible
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ER: 9159
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GENERAL INFORMATION:

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RESULT 6
US-08-715-106-10
Sequence 10, Application US/08715106
Patent No. 6020306
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                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein
US-08-702-367A-21
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INFORMATION FOR SEQ ID NO; 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 22; Conservative
                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                        Matches
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APPLICANT: FOX, GAIV M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/702,367A FILING DATE: CLASSIFICATION: 435
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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                                                                                                                        1 VNLLDSKTIQGELGWISYPSHG 22
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22; Conservat
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VENTION: EPH-Like Receptor Protein Tyrosine
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100.0%; Pr
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Pred. No. 1.7e-10;
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Pred. No. 1.7e-10;
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                                                                                                                                                                        Mismatches
                                                                                                                                                                                                     Length 983;
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RESULT 7
PCT-US95-04681-21
; Sequence 21, Application PC/TUS9504681
; GENERAL INFORMATION:
APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
ITILE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
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PRIOR APPLICATION NUMBER: PK9992 (AN APPLICATION NUMBER: PK9992 (AN APPLICATION NUMBER: PCT/AU92/NETION APPLICATION NUMBER: PCT/AU92/NETION DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION: NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
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APPLICANT:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 983 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acid
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
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APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOI
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 11530
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TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-21
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100. Matches 22; Conservative
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APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T; KROMER, LAWRENCE, F; VANDE WOUDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AN
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPE
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC CDOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 04-JAN-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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California
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TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
                                                                                                                                     08/177,812
                                                                                                                                                                                                             US/08/673,789
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                                         2026-4105
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Pred. No. 1.7e-10;
0; Mismatches 0;
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US-08-702-367A-30
; Sequence 30, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
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                                                                            RESULT 10
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: TELEX: 421792
: INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877
Type
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GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                 Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 967 amino acids
                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: EPH-Lik
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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APPLICANT: Fox, Gary M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
                                                                                                                                    1 VNLLDSKTIQGELGWISYPSHG
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o. 5981245
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T: 1840 Dehavilland Drive
Thousand Oaks
: California
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Similarity 63.6%;
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pred. No. 7.6e-06;
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Pred. No. 6.8e-06;
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RESULT 11
US-08-449-645A-13
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Best Local (
                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B:
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 967 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EPH-Like TITLE OF INVENTION: Kinases NUMBER OF SEQUENCES: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VNLLDSKTIQGELGWISYPSHG 22
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13 VNLLDSRTVMGDLGWIAFPKNG 34
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                       ZIP: 91320
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Local Similarity 63.6%;
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F: 1840 Dehavilland Drive
Thousand Oaks
              991 amino acids
amino acid
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linear
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Pred. No.
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-367A-13
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US-08-702-367A-13
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Best Local Similarity
Watches 14; Conserve
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                                                                                                                                                                             RESULT
                                                                                  Sequence 13, Application PC/TUS9504681
GENERAL INFORMATION:
APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Like Recep
TITLE OF INVENTION: Kinases
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Patent No. 5981246
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 991 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH
TITLE OF INVENTION: Kin
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
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                                                                      NUMBER OF SEQUENCES:
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CITY: Thousand Oaks
STATE: California
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ZIP: 91320
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                                                                                                                                                                                                                                      1 VNLLDSKTIQGELGWISYPSHG 22
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Thousand Oaks
California
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63.6%;
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                                                                                             EPH-Like Receptor Protein Tyrosine
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Pred. No.
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7.8e-06;
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Best Local S
Matches 14
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REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                       INFORMATION FOR SEQ ID NO:
                                                                                    REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-8674
TELEFAX: 415/952-9881
                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-CCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,2/
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
              SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acid
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
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Local Sim
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                              94080
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Similarity 63.6%; Pred. No.
14; Conservative 6; Mismatc
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emino acid
                                                                                                                                                                          Torchia, Timothy E.
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; TELEX: 910/371-7168; INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 928 amino acids TYPE: amino acid TOPOLOGY: linear US-08-440-815-2
Search completed: May
Job time: 4148 sec
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                                                                                                                                      Matches
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Best Local :
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APPLICATION NUMBER: US/08/440
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/330128
APPLICATION NUMBER: 08/330128
APPLICATION INFORMATION:
NAME: TOTCh1a, Timothy E.
REGISTRATION NUMBER: 35,700
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                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 92: TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.5e-05;
6; Mismatches :
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  W09300425-A.
07-JAN-1993.
19-JUN-1992. AU0294.
21-JUN-1991. AU-006841.
12-DEC-1991. AU-009992.
(HALL-) HALL INST MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins in modulating pre-B, B and T cell function, in cancer therapy etc.
Claim 6; Fig 1; 58pp; English.
This sequence represets human eph/elk-like kinase (HEK). HEK is expressed in both pre-B cells and T cell lines and in a number of tumours of human origin, eg. lymphoid tumours LK63, Lila-1 and JM, and the epithelial tumour HELA. This receptor-type thymidine kinase and the epithelial tumour HELA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer; expression vector; extracellular domain; human; HEK; eph/elk-like; kinase; pre-B; cell; T; tumour; lymphoid; LK63; Lila-l; JW; epithelial; HeLa; receptor-type; thymidine kinase; TK; ligand; B; cellular response; growth; differentiation.
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                                                                           Receptor type tyrosine kinase reactive with monocional antibody III-A4 - is EPH-ELK-like kinase, useful for phosphorylating proteins in modulating pre-B, B and T cell function, in cancer
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29-SEP-1998.
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04-JAN-1994; US-177812.
11-JUN-1996; US-673789.
(KROM/) KROMER L F.
(SCHU/) SCHULZ N T.
(WOUD/) WOUDE G F V.
(ZHOU/) ZHOU R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prognosis.
Gallus sp.
WO9515375-A.
                                                                                                                           Mouse Bsk receptor-like tyrosine kinase.

Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neoplasm; neurodegenerative disease; limbic system neuron regeneration; chromosomal abnormality; degenerative growth; development disorder; viral infection; bacterial infection; Alzheimer's disease; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 85-89; 129pp; English.

Probes derived from the EPH-related PTKs Cek4 (Q90659) and Ce (Q90660) were used to isolate novel cDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues and also in the adult brain and retina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasquale EB, Sajj
WPI; 95-215256/28.
N-PSDB; Q90659.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1995.
07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RES
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                                                                                            US5814479-A.
                                                                                                                  schizophrenia;
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                                Claim 18; Page 54-57; 133pp; English.

4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,

HEK8 and HEK11 (R85089-92), respectively, were identified following

1 isolation of their encoding cDNAs (702946-49) from a human foetal brain

1 cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the

2 catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8.

2 HEK11 shows no homology to any known EPH-like receptor. Recombinant

3 HEK receptors (or their soluble extracellular domains) are produced by

3 expression of encoding sequences in procaryotic or eucaryotic host

3 cells, and are used to produce antibodies (utilised in diagnostic

4 assays), or to identify and purify ligands for HEK receptors, or

5 therapeutically to modulate the activation of cell-associated

5 receptors. Soluble HEK7 receptor may primarily affect

5 proliferation and/or differentiation of brain cells.
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Claim 18;
4 Novel hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents mouse Bsk, which is a receptor-like tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in Bsk nucleic acid probes, which can be used in detecting alterations is the level of Bsk messenger-RNA (mRNA) in biological samples isolated from a mammal afflicted with a disease, such as neurodegenerative diseases or disorders and neoplasms. The nucleic acid sequence can albe delivered into the limbic system of patients with limbic system neurodegenerative disease, disorder or injury, to promote or enhance limbic system neuron regeneration or growth. Such neurodegenerative diseases include, chromosomal abnormalities, degenerative growth and development disorders, viral infections, bacterial infections, brain injuries, neoplastic conditions, Alzheimer's disease, epilepsy, schizophrenia, or stroke and cerebral ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid sequence encoding protein - used in nucleic acid probes, used in detecting alterations in lever messenger-RNA in biological samples isolated from mammal a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kromer LF, Schulz NT, Woude GFV, WPI; 98-541751/46.
N-PSDB; V58192.
                                                                                                                                                                                                                                                                                                        New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPH-like receptor protein tyrosine kinase HEK7 EPH-like receptor protein tyrosine kinase; PTK human eph-like kinase; therapy; diagnosis; vec
                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
Ting S, Welcher AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO sapiens.
WO9528484-A1.
                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T02947
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-1995; U04681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R85090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 2; 72pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with disease
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1994; US-229509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l6-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VNLLDSKTIQGELGWISYPSHG
||||||:|: |:||||::| :|
63 VNLLDSRTVMGDLGWIAFPKNG
                                                                                                                                                                                                                                                                                                                                                                                     3M, Jing S,
95-373799/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
 cells.
991 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or stroke AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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5.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTK; HEK7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s in level of Bsk
mammal afflicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Matches 14; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment and diagnosis of neuronal disorders and angiogenesis-related conditions.

Example 1; Page 50-53; 75pp; English.

Rat REK7 (R97853) is an eph-related tyrosine kinase receptor, for which AL-1 (see also W97854) is a ligand. Its amino acid sequence was deduced from a cDNA clone (T18893) isolated from a hippocampal cDNA library. An REK 19G fusion was used to screen cultured cell lines for surface expression of REK7-binding activity. Primers (see also T44382-83) based on peptide sequences (R97856-59) of isolated ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human foetal brain cDNA library, leading to the isolation of AL-1 cDNA contacts.
  01-DEC-1998.
06-JUN-1995;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1995;
27-OCT-1994;
07-JUN-1995;
                                                                                                         Rat receptor tyrosine kinase Ehk-1.
Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; neurotrophin activity; trkB; proto-oncogene; tyrosine binding protein; BDNF; NT-3; diagnosis.
                                                                                                                                                                                                                            W83147 standard;
W83147;
                                                                   Rattus sp.
US5843749-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caras IW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REK7; eph-related tyrosine kinase receptor; AL-1; ligand; neurotrophic factor; neuropathy; anglogenesis; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat REK7
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R97853;
                                                                                                                                                                                                         11-FEB-1999
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-1994; US-330128.
-1995; US-486449.
) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eph-related tyrosine kinase receptor.
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469537.
US-406247.
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58. .462
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                                                                                                                                                                                                                                                 Protein;
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63.6%;
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6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; ....
.. 1.1e-05; 2;
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1 VNLLDSKTIQGELGWISYPSHG

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Example; Fig 22; 194pp; English.

The present invention describes nucleic acid molecures are ror-2, ehk-1 and ehk-2. Also described are the corresponding prot Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence represents rat Ehk-1.
                                               domain and Ig constant domain, useful for studying, and therapeutic modulation of, cell growth and differentiation
Disclosure; Page 95-99; 125pp; English.
DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify novel pTK genes. The bpTKS, bpTK3, bpTK4, bpTK5 and bpTK7 (R85924-28 and R85935, respectively) are expressed in human brain tissue and show homology to known pTKs. A full-length sequence for bpTK7 (R85936) was also obtd. bpTK7 can be used to design drugs that modulate pTK activity.
                                                                                                                                                                                                                                     12-OCT-1995.
04-APR-1995;
04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1991;
28-OCT-1993;
06-JUN-1995;
                                            obtd. bpTK7
Sequence 98
                                                                                                                                         Agonist antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic
                                                                                                                                                                                                     Wood
                                                                                                                                                                                                               Bennett
                                                                                                                                                                                                                                                                       W09527061-A1.
                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                            Protein tyrosine-kinase Protein tyrosine-kinase; differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding
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Maisonpierre PC, Masiakowski P,
                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                       domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  R85936 standard;
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                                                                                                                                                                                                                          (GETH )
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14; Conser
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; US-144992.
; US-469537.
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                                            can be used
86 AA;
                                                                                                                                                                                                                          US-222616.
NTECH INC.
                                                                                                                                                                                                                                               U04228
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                                                                                                                                                                                                               Goeddel
                                                                                                                                                                                                                                                                                         548. .570 /label= Transmembrane_domain 571. .986
                                                                                                                                                                                                                                                                                                                /label= Extracellular_domain 548. .570
                                                                                                                                                                                                                                                                                                                                         1. .19
/label=_Sig_peptide
                                                                                                                                                                                                                                                                               571. .986
/label= Ir
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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 66.4%;
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                                                                                                                                                                                                                                                                               Intracellular_tyrosine-kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                   bpTK7
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                                                                                                                                                                                                               Lee
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                                                                                                                                                                                                              Matthews W,
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Best Local S
Matches 14
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06-JUN-1995; 469537.

17-MAR-1995; US-406247.

26-JUL-1991; US-736559.

28-OCT-1993; US-144992.

06-JUN-1995; US-469537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7 HEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (T02946-49) from a human foetal br cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced expression of encoding sequences in procaryotic or eucaryotic host cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HEK receptors, or therepoutlically to modulate the activation of cell-associated
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Claim 18; Page 62-65; 133pp; English.
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       proteins
Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; neurotrophin activity; trkB; proto-oncogene; tyrosine binding protein; BDNF; NT-3; diagnosis.
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                                                                                                                                                  (REGE-) REGENERON PHARM INC. Maisonpierre PC, Masiakowski WPI; 99-044584/04.
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EPH-like receptor protein tyrosine kinase; PTK; HEK8;
human eph-like kinase; therapy; diagnosis; vector; an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R85091 standard; Protein; R85091;
                                                                           DNA encoding
                                                                                                                        N-PSDB; V70208
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W83148;
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Sequence
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L5-APR-1994; US-229509.
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receptor tyrosine kinase Ehk-2
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diagnosis.
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kinase receptor;
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Best Local Similarity 59...
Matches 13; Conservative
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Embryonic stem cell kinase (Esk).
Embryonic stem cell kinase; receptor
Embryonic stem cell kinase; receptor
epithelium; signal transduction; gene
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RESULT
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ID RE
AC RE
DT 16
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                                                                                                                                                                                                                     PT DNA encoding embryonic stem cell kinase, receptor tyrosine kinase - production of modulators and antibodies, useful to treat mucositis and other disorders involving epithelium Claim ; page 48-54; 98pp; English.

Novel mouse embryonic stem cell kinase (Esk) is a receptor tyrosine kinase that belongs to the Eph subfamily. Its amino acid sequence was deduced from a DNA molecule (T72320) isolated from a murine liver cDNA library. Recombinant Esk polypeptides, esp. soluble Esk (extracellular domain), can be produced in host cells and used for ligand isolation, as antagonists of Esk-ligand interaction and as immunogens for prodn. of antibodies useful as diagnostic reagents or therapeutic antagonists of Modulation of Esk expression can be used to treat mucositis (partic. when caused by cancer treatment), and as Esk is expressed in all epithelial tissues its modulation may be used to treat e.g. skin injuries, hair loss, corneal or peptic ulcers, ulcerative colitis, oesophageal reflex, sjorgren's syndrome and related autoimmune disease, mucosal infections and pancreatitis.
                                                                                                                                               Matches
                                                                                                                                                           Query Match
Best Local
R85092 standard; Protein; 998
R85092;
16-APR-1996 (first entry)
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03-JUL-1997.
20-DEC-1996; AU0826.
22-DEC-1995; AU-007277
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AIP binding motif"
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/note- "GXGXXG ATP |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= ATP-binding_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Fibronectin_type-III_repeat
/note= "characteristic of Eph subfamily"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Fibronectin_type_III_repeat
/note= "characteristic of Eph subfamily"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label- Glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Glycosylation
/note= "potential N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-
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                                                                                                                                                       52.1%;
57.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "potential
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Pred.
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                                                                                                                                                        No. 0.
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binding motif"
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0.11;
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                                                                                                                                                                    Length
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                                                                                                                                                                      977;
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Best Local
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11-JUL-1996.
03-JAN-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES FC
(SUGE-) SUGEN INC.
Clossek T. Millauer B,
WPI; 96-333988/33.
N-PSDB; T32961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7 HEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (T02946-49) from a human foetal brodna library. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced expression of encoding sequences in procaryotic or eucaryotic host cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HEK receptors, or therapeutically to modulate the activation of cell-associated
                                                                                                                                                                                                                                                                                                                   Mouse developmental kinase 1 MDK1 T1.

Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase; RTK; signal transduction; probe; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                      W03422
                                                                                                         WO9621013-A1.
                                                                                                                                   misc_difference
                                                                                                                                                                                     modified_site
                                                                                                                                                                                                                modified_site
                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                         neurodegeneration; neuroproliferation; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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14-APR-1995; U04681.
15-APR-1994; US-229509.
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WO9528484-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPH-like receptor protein tyrosine kinase HEK11.
EPH-like receptor protein tyrosine kinase; PTK; HEK11;
human eph-like kinase; therapy; diagnosis; antibody; vector.
                                                                                                                                                                                                                                                                                            Mus sp.
                                                                                                                                                                                                                                                                                                                                                             11-NOV-1996
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95-373799/48.
                                                                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid encoding EPH-like receptor tyrosine kinase(s) vectors, host cells, proteins, antibodies etc., uslly and therapeutically to modulate receptor activa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N INC.
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                                                                                                                                                                                    /label= N-glycosylation_site
343 .345
/label= N-glycosylation_site
410 412
                                                                                                                                    600.
                                                                                                                                                                                                                                         /label= Sig_peptide
64. .66
                                                                                                                      /note=
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                               label-
                                                                                                                                                                          /label=
                                                                                                                                    .610
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63.6%;
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.579
                                                      FOERDERUNG WISSENSCHAFTEN
                                                                                                                     "product of alternative splicing"
                                                                                                                                                Transmembrane_domain
                              Ullrich
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CDNA cloning using adult mouse brains and Northern blotting clonary clonary controls, MDK1 T1 (W03422) and MDK1 T2 (W03423), of the novel mouse developmental kinase 1 (MDK1) (see also C (W03421), a new member of the eck/eph family of receptor tyrosine c kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential signal transduction.

Sequence 610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conser
          Example 1; Page 113-115; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting identified 2 truncated versions, MDKI T1 (W03422) and MDKI T2 (W03423), of the novel mouse developmental kinase 1 (MDKI) (see also W03421), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mouse diagnosis
                                                                                                                                                                New mouse development kinase 1 gene - used for developing prods. diagnosis and treatment of abnormalities in signal transduction pathways
                                                                                                                                                                                                                           11-JUL-1996.
03-JAN-1996; U00419.
03-JAN-1995; U5-368776.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
(SUGE-) SUGEN INC.
C10ssek T, Millauer B, Ullrich A;
WPI; 96-333988/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse developmental kinase 1 MDK1 T2.
Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase;
RTK; signal transduction; probe; diagnosis; gene therapy;
                                                                                                                                                                                                             N-PSDB; T32962
                                                                                                                                                                                                                                                                                                                                                              misc_difference
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/label= N-glycosv'-...
555. .570
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600. .(
/note-
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treatment of diseases
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_345
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                                                                                                                                                                                                                                                                                                                                             "product of alternative splicing"
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Pred. No.
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ies in signal transduction
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0.19;
characterised
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                                            Query Match
Best Local S
Matches 14
                                                                                                 Example 1: Page 105-108; 128pp; English.

12 Mouse developmental kinase 1 (MDK1) (W03421) is a new member of the ceck/eph family of receptor tyrosine kinases (RTKs). Its amino cack/eph family of receptor tyrosine kinases (RTKs). Its amino acid sequence was deduced from a cDNA clone (T32960) isolated from mouse embryo and adult brain libraries. The distinct patterns of MDK1 expression during mouse development suggest an important role for MDK1 in the formation of neuronal structures. MDK1 may be obtd. by expression in host cells. It can be used in methods for the diagnosis of diseases characterised by abnormality in a signal transduction pathway, such as neuroproliferative or neurodegenerative disorders or cancer, to screen for (ant)agonists, and to raise antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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03 JUN-1996; U00419.
03 JUN-1995; US-368776.
(PLAC ) MAX PLANCK GES F
(SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
Key
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Mouse developmental kinase 1.
Mouse developmental kinase 1; MDK1; receptor tyrosine kinase; RTK;
signal transduction; probe; diagnosis; therapy;
neurodegeneration; neuroproliferation; cancer.
                                                                                                                                                                                                                                                       New mouse development kinase 1 gene - use diagnosis and treatment of abnormalities pathways
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_site
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Sequence 626 AA;
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N-PSDB; T32960.
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                   1 VNLLDSKTIQGELGWISYPSHG
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VLLLDSKAQQTELEWISSPPSG
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14; Conservative
                                                       Similarity
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                                            Conservative
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555. .5
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                                          Score 59; DB
Pred. No. 0.33
0; Mismatches
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RESULT W19968 ID W1

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W19968

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DR N-PSDB; 771086.

PT Imman and yeast alanyl-tRNA synthetase genes - useful for production of recombinant enzymes for diagnostic and analytical applications PS Claim 3; Column 43-48; 42pp; English.

CC W19968 shows the amino acid sequence of human alanyl-tRNA synthetase CC (Ala-tRS). Human Ala-tRS and antibodies specific for it, may be useful CC in assays for diagnosing and monitoring an autoimmune disease known as CC antisynthetase syndrome. A condition in which patients having CC polymyositis and/or dermatomyositis produce antibodies against the cessential synthetase enzyme. Anti-synthetase syndrome is characterised by a number of clinical presentations, including interstitial lung CC disease, arthritis, Raynaud's phenomenon and fever. Human Ala-tRS can be used to assess the toxic effects of antimicrobial Ala-tRS can CC of such antimicrobial agent which complements or substitutes the CC function of the native gene can be used to test for any toxic effects of such antimicrobial agents that specifically interacts with the human CC Ala-tRS gene or protein. Ala-tRS proteins can be used to separate CC alanine from other amino acids, to separate L-alanine from D-alanine, CC quantitative determination of alanine or ATP.
                                                                                                                                                                        Query Match
Best Local Similarity 47.1
Matches 10; Conservative
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21-APR-1995; 426236.
21-APR-1995; US-426236.
(CANC-) CANCER INST JAPANESE FOUND CANCER.
(CUBI-) CUBIST PHARM INC.
(MASI ) MASSACHUSETTS INST TECHNOLOGY.
Ripmaster TL, Schimmel PR, Shiba K;
WPI; 97-280271/25.
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Human alanyl-tRNA synthetase.
Alanyl-tRNA synthetase; ligase; analysis; diagnosis; autoimmune;
disease; antisynthetase syndrome; interstitial lung disease;
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Pred. No. 0.
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11: sp_virus:
12: sp_virus:
13: sp_verteb
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Match
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Gapop 10.0 ,
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Q76154

Q81224

Q81225

Q81462

Q23683
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       09zvs8 arabidopsis
09y0y9 drosophila
09z330 rattus ratt
094559 schizosacch
018215 caenorhabdi
088893 tobacco rin
081339 mesembryant
019445 caenorhabdi
P73491 synechocyst
P91851 caenorhabdi
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076154 dugesia jap
081224 arabidopsis
081225 arabidopsis
081225 arabidopsis
080462 arabidopsis
020643 caenorhabdi
020523 caenorhabdi
027520 methanobact
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homo sa	2	<u> </u>	Q9yhd9 brachydanio		O81887 arabidopsis			Q9z6f5 vibrio para		n	Q85538 feline immu			œ	chlan	Q13816 homo sapien		Q96891 hog cholera	chol	P79922 xenopus lae	Q66960 feline immu		P79333 oryctolagus	Q9x958 streptomyce

ALIGNMENTS

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X MELSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

XA MILSON R., DIRCOUGH R., ANDERSON K., CODSEX T., COOPER J., COULSON A.,

XA DONFIELD J., BURTON J., CONNELL M., CODSEX T., COOPER J., COULSON A.,

XA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

XA JONES M., KERSHAW J., KIRSTEN J., LAITSEILLE P.,

XA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

XA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

XA THIERRY-MIEG J., THOMAS K., VAUDLN M., VAUGHAN K., WATERSTON R.,

XA THIERRY-MIEG J., THOMAS K., VAUDLN M., VAUGHAN K., WATERSTON R.,

XA THIERRY-MIEG J., THOMAS K., VAUDLN M., VAUGHAN K., WATERSTON P.;

YI 2.2 MD of contiguous nucleotide sequence from chromosome III of C.

YI 2.2 MD of contiguous nucleotide sequence from chromosome III of C.

YI 2.35595; CA884634.1; -.

XE EMBL; Z35595; CA884634.1; -.

XE EMBL; Z35595; CA884634.1; -.
                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conser
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01-NOV-1996 (TIEMBLIEL 0
01-NOV-1996 (TIEMBLIEL 0
01-JAN 1999 (TIEMBLIEL 0
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Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhai
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105 IDFQMRLLILLICSAFSTCSVLDSFRANGIEFEVYGEGRLIPE
                                                  .3 PROTEIN
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                                                                                                                                                        Conservative
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Rhabditidae; Peloderinae; Caenorhabditis
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Pred. No. 0.
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O76154;
O76154;
O1-NOV-1998 (Tremblrel. 08, L;
O1-NOV-1999 (Tremblrel. 12, L;
NA+/K+-ATPASE ALPHA-SUBUNIT.
DJNAK.
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PFAM; PF00689; Na_K_ATPASS_C; 1.
PFAM; PF00690; Na_K_ATPASS_N; 1.
PFANTS; PR00119; CATATPASE.
PRINTS; PR00112; NAKATPASE.
PRINTS; PR00121; NAKATPASE.
SEQUENCE 1022 AA; 113462 MW; 8
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euphyllophytes;
core eudicots; R
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O81224;
O1-NOV-1998
O1-NOV-1999
O1-NOV-1999
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
LEE Y.-R.J., ASSMANN S.M.;
"Arabidopsis thaliana extra-large G-protein: a new class binding protein.";
binding protein.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; APG60941; AAC19352.1;
HSSP; P10824; 1BH2.
PFAM; PF00503; G-alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
EMBL; AB013391; BAA32798.1; -.
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OGATA S., WATANABE K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dugesia japonica (Planarian).
Eukaryota; Metazoa; Platyhelminthes;
Paludicola; Dugesiidae; Dugesia.
                                                                                                                                                                                                                   SEQUENCE
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DCELSSSGELLLRSCSVKESLDLNESSSNPLVPDWESNE
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7; Conserv
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(TTEMBLrel. 08, Last sequence up
(TTEMBLrel. 12, Last annotation
G-PROTEIN.
                                                                                             Conservative
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AA; 98796 MW;
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43.6%;
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STRAIN-CV. KAUL S., LIN X., KETC ROUNSLEY S.D., KAUL S., LIN X., KETC BRANDON R.C., SYKES S.M., MASON T.M. SOMERVILLE C.R., VENTER J.C.;
I "Arabidopsis thaliana chromosome II submitted (JUN-1998) to the EMBL/Ge EMBL; ACO03040; AAC23761.1; -.
IR EMBL; ACO03040; AAC23761.1; -.
IR HSSP; B10824; 1A52.
JR PEAM; PF00503; G-alpha; 1.
DR PEAM; PF00503; G-alpha; 1.
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
EXTRA-LARGE G-PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PUTATIVE GUANINE NUCLEOTIDE-BINDING PROTEIN.
F2685.11.
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STRAIN-CV. LANDSBERG;
LEE Y.-R.J., ASSMANN S.M.;
Parabidopsis thaliana extra-large G-protein: a new class binding protein.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF660942; ARC19353.1; -.
HSSP; P10824; 1BH2.
PFAM; PF00503; G-alpha; 1.
SEQUENCE 888 AA; 98860 MW; 3F6B542C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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DCELSSSGELLLRSCSVKESLDLNESSSNPLVPDWESNE
                           DCQLSI---LLLLSCSVLDSF-----GELIPQ-PSNE
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17; Conserv
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17; Conser
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nilarity 43.6%;
Conservative
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ilarity 43.6%;
Conservative
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EMBL/GenBank/DDBJ
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                                                                                         Score 49.5; D
Pred. No. 23;
3; Mismatches
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T.M., KERLAVAGE
                                                                                                                                                                                                              93E6ED24 CRC32;
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154
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GE A.R., ADA
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                                                                                                                                                                                                                                                                                                             genomic sequence.";
databases.
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A GONNELL M., COPERY T., COOPER J., COULSON A., A., COPARY T., COOPER J., COULSON A., A., CRAYGON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L., A., CRAYGON M., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., A., JONES M., KERSHAM J., KIRSTEN J., LATREILLE P., JONES M., KERSHAM J., KIRSTEN J., LATREILLE P., JONES M., KERSHAM J., KIRSTEN J., LATREILLE P., COLLIAGHAN M., A., LIGHTWING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNEEN R., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNEEN R., RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDWAN P.;

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDWAN P.;

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDWAN P.;
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Best Local S
Matches 9
Submitted (AUG-1998) to the E
EMBL; AP083043; AAD28102.1; -
EMBL; AF083038; AAD28102.1; J
EMBL; AF083039; AAD28102.1; J
EMBL; AF083040; AAD28102.1; J
EMBL; AF083041; AAD28102.1; J
                                                                                          MEDLINE; 98389/05.

DENG J., SZYF M.;

"Multiple isoforms of DNA methyltransferase are vertebrate cytosine DNA methyltransferase gene."

Phiol. Chem. 273:22869-22872(1998).
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01-NOV-1996
01-JAN-1999
                                                                                                                                                                                                                                                        Q9WTX3;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE;
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BERKS M.;
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Q23683;
                                                                            SEQUENCE FROM N.A. DENG J., SZYF M.;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOSINE DNA METHYLTRANSFERASE (FRAGMENT).
                                                                                                                                                                                                         Eutheria; Rodentia;
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                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                               Q9WTX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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EMBL; Z49073; CAA88891.1;
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94150718.
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Pred. No.
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thi; Muridae; Murinae;
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Best Local Similarity
Matches 10; Conser
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MEDLINE; 94150718.
WILSON R., AINSCOUGH R
BONFIELD J., BURTON J.
                                                                                                027520
027520;
01-JAN-1998
01-JAN-1998
01-NOV-1999
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01-JAN-1998
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WATSON A., "2.2 Mb of elegans.";
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., CALLAGHAN M.
PARSONS J., PERCY C., RIFKEN L., ROOPAA A., SUNDERS D., SHOWNKEE
SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
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EMBL; Z83102; CAB05466.1;
SEQUENCE 399 AA; 46244
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Transferase; Methyltransferase.
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NON_TER 349 349
SEQUENCE 349 AA; 39021 MW; CCB:
                                      Methanobacterium
                                                           MTH1476
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Eukaryota; Metazoa; Nem
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C54C8.4.
  Methanobacterium
                   Archaea;
                                                                               TRYPTOPHAN
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8; Conservative
                   Euryarchaeota;
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18 (TrEMBLrel. 0
19 (TrEMBLrel. 1
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illarity 62.5%;
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Nidea; Rhabditidae; Peloderinae; Caenorhabditi
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                                                                                                                                                                                 PRT;
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annotation
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ALDREDGE T., BASHIRZADER R., BLAKELY D., COOK R., GILBERT K.,
ALDREDGE T., BASHIRZADER R., BLAKELY D., COOK R., GILBERT K.,
ALDREDGE T., BASHIRZADER R., EAGLE P., LUMM W., POTHIER B., QIU D.,
AND ALDREDGRA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
AND JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
AND ALDREDGE C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
TOMPLETE Genome sequence of Methanobacterium thermoautotrophicum
of deltaH: functional analysis and comparative genomics.";
J. Bacteriol 179:7135-7155(1997).
BR EMBL, AED00098; AAM85951.1;
BR PFAM; PF00933; 2WSY.
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Best Loc
Matches
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STRAIN-CY COLUMBIA;

VYSOTSKAIA V.S., SCHWARTZ J.R., TORIUMI M., YU G.,

VYSOTSKAIA V.S., SCHWARTZ J.R., TORIUMI M., YU G.,

VYSOTSKAIA V.S., SCHWARTZ J.R., DURUER E.,

ERREMETSKAIA I., LUROS J., ARAUJO R., SUN H.,

DEWER K., FENG J., KIM C., LI Y., SHINN P., SUN H.,

ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;

"ATABIOODSIS thallana chromosome 1 BAC F15K9 sequer

"ATABIOODSIS thallana chromosome 1 BAC F15K9 sequer

"ATABIOODSIS thallana chromosome 1 BAC F15K9 sequer
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SEQUENCE FROM
STRAIN-DELTA
    MENDEL; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
euphyllophytes; Rosidae; eurosids II; Brassicales; Brassicaceae;
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01-NOV-1999
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MEDLINE; 98037514.
                                             Submitted (NOV-1998) to the EMBL/GenBank/DDBJ EMBL; AC005278; AAC72127.1; -.
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    38431;
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14; Conservative
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AA; 47487 MW;
  Arath;3293;38431
AA; 56415 MW;
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27;
    CRC32;
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., DAVIS
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Q9Y0Y9
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Matches
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ROBIN G.M., WAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG AGBAYANI A., ARCAINA T.T., BAXTER E., BLAZEJ R.G., BUTENHOFF C., CHAMPE M., CHAVEZ C., CHEW M., DOYLE C.M., FARFAN D.E., FRISE E., GALLE R., GEORGE R.A., HARRIS N.L., HOSKINS R.A., EVANS-HOLM M., HOUSTON K.A., HUMMASTI S.R., KIM E., LI P., MOSHREFI M., PACLEB (CELNIKER S.E.; SEQUEIRA A., SETHI H., SNIR E., SVIRSKAS R.R., WEINBURG FULL Length DICOSOphila melanogaster CDNA sequence.";

SUBMITTED (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF145687; AAD38662.1; -.

SEQUENCE 1146 AA; 124541 MW; 8DA1D02B CRC32;
                                                                                                                                                             "Expression of rat DNA (cytosine-5) methyltransferase rodent trophoblast giant cells: molecular cloning and of rat DNA MTase.";
Biochem. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Z330;
Q9Z330;
                Biochem. Biophys. Res. Commun. 253:495-501(1998).
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + I
ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.
-!- SIMILARITY: STRONG, TO OTHER C5-DNA METHYLASES.
EMBL; AB012214; BAA37118.1; -
PROSITE; PS00094; C5_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
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01-MAY-1999 (TrEMBLrel. 10,
01-NOV-1999 (TrEMBLrel. 12,
MODIFICATION METHYLASE (EC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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01-NOV-1999
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TISSUE-BRAIN, AND PLACENTA;
MEDLINE; 99097263.
KIMURA H., TAKEDA T., TANAK
                                                                                                                                                                                                                                                                                                                                                           METHYLTRANSFERASE).
Rattus rattus (black rat).
Eukaryota; Metazoa; Chorda
Eutheria; Rodentia; Sciuro
  Transferase;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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9; Conserv
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    Methyltransferase;
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Sciurognathi; Muridae;
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ae; Murinae;
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a; Brachycera; Muscomorpha;
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                  SEQUENCE FROM N.A.
MEDLINE; 94150718.
WILSON R., AINSCOUGH F
BONFIELD J., BURTON J.
   CRAXTON GARDNER
                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
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018215;
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ
EMBL; 299753; CAB16876.1; -
Hypothetical protein.
SEQUENCE 431 AA; 49532 MW; 67F4D4CF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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SEQUENCE
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01-JAN-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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STRAIN-972H-;
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01-MAY-1999 (TrEMBLrel.
HYPOTHETICAL 49.5 KD PRC
SPAC23C4.05C.
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Y53C12B.1.
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Submitted (OCT-1997) to
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J., LENNARD N
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R., ANDERSON K., BAYNES C., BERKS M.,
CONNELL M., COPSEY T., COOPER J., COU
Z., DURBIN R., FAVELLO A., FULTON L.,
HAWKINS T., HILLIER L., JIER M., JOHNS
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A LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAI
A PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWL
A SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
A THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON J.
A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
T "2.2 Mb of contiguous nucleotide sequence from chromosome III
T elegans.";
L Nature 368:32-38(1994).
R REMBL; 279278; CAB16490.1; -.
R PFAM; PF00400; WD40; 6.
R PRINTS; PR00320; GPROTEINBRET.
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Q88893;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                         genomic RNAs and characterization Virology 219:1-8(1996).
EMBL; U50869; AAB03785-1; -.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PFAM; PF00910; RNA_helicase; 1.
                                                                                                             1775
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ZALLOUA P.A., BUZAYAN J.M., BRUI
"Chemical cleavage of 5'-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BUD BLIGHT; MEDLINE; 96204566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA1 POLYPROTEIN.
Tobacco ringspot virus (Tobrsv) (Trsv).
Viruses, ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                       SEQUENCE 2
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PRINTS; PRO0014; ENTYPEIII.
PRINTS; PRO0109; TYRRINASE.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
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RA Sajjadi F.G., Pasquale E.B., Subramani S.;

RA Trong Mentification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor.";

RA Least two forms of the receptor.";

RI New Siol. 3:769-778(1991).

C. -I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO C. EPHRIN-A2, -A3, -A4 AND -A5.

C. -I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO C. -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PFAM; PF00041; fn3; 2.

PFAM; PF00069; pkinase; 1.

PFAM; PF00069; pkinase; 1.

PFAM; PF001404; EPH_lbd; 1.
                                                  O08680;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-FEB-2000 (Rel. 39, Last annotation update
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.
KINASE RECEPTOR REK4).
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CARBOHYD
VARSPLIC
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MOD_RES
CARBOHYD
CARBOHYD
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BINDING
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
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EMBL; M68515; AAA39522.1; ALT_SEQ.
PIR; A45583; A45583.
HSSP; P16109; 1F5B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electric Control of Bioinformatics and th
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DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                              EPHA3 OR REK4
                                                                                                                                                                                                                                                                                                                                 EPA3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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    Rattus
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norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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BY SIMILA
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POTENTIAL.
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1; Mismatches
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ATP (BY SIMILA
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FIBRONECTIN TYPE-III.
PROTEIN KINASE.
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oprotein; Signal; Alternative splicing
BY SIMILARITY.
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                                                                                                                  update)
C 2.7.1.112) (TYROSINE-PROTEIN
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Query Match
Best Local s
Matches 19
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
PROSITE; PS001796; GEC=2; UNKNOWN_1.
PROSITE; PS001796; GEC=2; UNKNOWN_1.
PF0AM; PF00041; fn3; 2.
PFAM; PF000536; SAM; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                                                     MOD_RES
CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                                  DOMAIN
NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li Y.Y., McTiernan C.F., Feldman A.M.;
"IL-1 beta alters the expression of the receptor r-EphA3 in neonatal rat cardiomyccytes.";
Am. J. Physiol. 274:H331-H341(1998).
-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-EPHRIN-A2, -A3, -A4 AND -A5.
-i- CATALYTIC ACTIVITY: AIP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U69278; AAC06273.1; -HSSP; P16109; 1FSB.
PRINTS; PRO0014; FNTYPEIII.
PRINTS; PRO0109; TYRKINASE.
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Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SPRAGUE-DAWLEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                     MDCQLSILLLLSCSVLDSFGELIPQPSNE
MDCHLSILILFGCCVLSCSRELSPQPSNE
                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC06273.1; -.
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RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                        110227
                                                                                          63.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                                                                                     ¥,
                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
                                                                      1;
                                                                      Score 94; DB Pred. No. 3.1e 1; Mismatches
                                                                                                                                                             POTENTIAL.
POTENTIAL.
v; F170C49312F7A0AB CRC64;
                                                                                                                                                                                                                        ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase; ATP-binding; Phosphorylation;
                                 29
                                                                                                            DB 1;
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                                                                                                          Length 984
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RESULT 5
Y091_NPVAC STANDARD; 1
AC P41479;
DT 01-NOV-1995 (Rel. 32, Created)
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Best Local S
Matches 13
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SIGNAL 1 29
CHAIN 30 500
REPEAT 30 226
DOMAIN 227 267
REPEAT 268 457
DOMAIN 471 499
DISULFID 39 225
DISULFID 39 225
DISULFID 231 242
DISULFID 231 242
DISULFID 238 251
DISULFID 238 266
DISULFID 253 266
CARBOHYD 80 80
CARBOHYD 80 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, sequence,";
matrix protein cDNA.";
Eur. J. Biochem. 236:970-977(19
-i-FUNCTION: CARTILAGE MATRIX
-i-FUNCTION: MATRIX OF NON
                                                                                                                                                                                     DOMAIN
DISULFID
DISULFID
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; C
Eutheria; Rodentia; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARTILAGE MATRIX PROTEIN PRECURSOR MATN1 OR CRIM OR CMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence ul)
15-DEC-1998 (Rel. 37, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P51942;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:106591; MATN1.
PRINTS; PR00453; VWFADOMAIN.
PROSITE; PS00022; EGF_1; FAI
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
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MEDLINE; 96270751.
                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00008; EGF; PFAM; PF00092; vwa;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U35035;
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                                                                                                      3 CQLSILLLLSCSVLDSFGELIPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMOTRIMER (BY SIMILARITY) SIMILARITY: CONTAINS 1 EGF-LIKE DOM
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                                                                                 CSLLLLLLLLQVPDSL-SLVPQP
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                                                                                                                              Conservative
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                                                                                                                                                                                       54446
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POTENTIAL.
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POTENTIAL.
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POTENTIAL.
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Pred. No. 2
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POTENTIAL.
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CMP 1.
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Mus.
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RESULT 6
EPA3_C
ID 3_CHICK
ID 3_CHICK
ID 10-DEC
DT 01-DEC
CO EVARY
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RN [1]
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETKI) (CEK4)
EPHA3 OR ETKI OR CEK4.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 92031278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L22858; AAA66721.1; -.
Hypothetical protein.
SEQUENCE 224 AA; 24138 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete DNA sequence of polyhedrosis virus."; Virology 202:586-605(1994).
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Viruses; dsDNA viruses,
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01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTE
Autographa californica nuclear polyhedrosis v
                                                                                               -1- SIMILARITY: CONTAINS
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                                                                                                                                                                                        FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRAN TISSUE SPECIFICITY: GREATEST LEVELS
                                                                                                                     SIMILARITY: TO COMMIN. BELONGS
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                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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10; Conservative
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; Galliformes;
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    Swiss Institute
Bioinformatics
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                                                                                     TO OTHER PROTEIN-TYROSINE KINASES IN THE CAT. DNGS TO THE EPHRIN RECEPTOR FAMILY. CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
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ce of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phasianidae;
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ianidae; Phasianinae; (
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RESULT 7
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DT 15-JUL
DE METHYL
GN DNMT.
OS MUS mU
OC EUKher
RN [1]
RP SEQUEN
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RT mouse
RT relate
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Best Local S
Matches 11
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.

PFAM; PF000069; Pkinase; 1.

PFAM; PF000053; SAM; 1.

PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                      P13864;
01-AN-1990 (Rel. 13, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
DNA (CYTOSINE-5) METHYLTRANSFERASE (EC 2.1.1.37)
DNA (CYTOSINE-5) (DNA METASE) (MCMT) (M.MMUI).
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CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
Bestor T.H., Laudano A., Mattaliano R., Ingram V.; "Cloning and sequencing of a cDNA encoding DNA methyltransf mouse cells. The carboxyl-terminal domain of the mammalian related to bacterial restriction methyltransferases."; J. Mol. Biol. 203:971-983(1988).
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MOD_RES
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DOMAIN
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PIR; B45583; I
                                                            SEQUENCE FROM N.A. MEDLINE; 89094873.
                                                                                                                        Mus musculus (Mouse).
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Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 19 BY SIMILARITY.
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an email to license@isb-sib.ch).
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Sciurognathi; Muridae; Murinae;
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1; E8895F0BDF77651E CRC64;
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ATP
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                                                                                                                                                                                                                                                                                                                                                       Length 983;
                                     methyltransferase
                                                                                                                                                           (DNA
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                  Mus
                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
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RESULT
INA1_PIG
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Best Local S
Matches 8
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PIR; S01845; S01845;
REBASE; RE02813; M.MmuI.
MGD; MGI:94912; Dnmt.
MGD; MGI:94912; Dnmt.
PRINTS; PR00105; CCMETTRERASE.
PRINTS; PR00105; CS_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
PROM: PF00145; DNA_methylase; 3.
                                                                                                                                                                                                                                             INA1_PIG STANDARD; PRT; 189 AA P49879; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update INTERFERON ALPHA-1 PRECURSOR (IFN-ALPHA-1). Sus scrofa (Pig).
 SEQUENCE FROM N.A.
MEDLINE; 87035119.
Lefevre F., la Bonnardiere C.;
"Molecular cloning and sequencing of a active porcine alpha-interferon.";
J. Interferon Res. 6:349-350(1986).
-!- FUNCTION: PRODUCED BY MACROPHAGES,
                                                                                                                                                                                                                                                                                                                                                                                                         1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -I- FUNCTION: METHYLATES CG RESIDUES.

I- CAPALYTIC ACTIVITY: S-ADENOSYL-I-ETHIONINE + DNA
HOMOCYSTEINE + DNA CONTAINING 5-METHYLCYTOSINE.

I- SIMILARITY: HIGH, TO OTHER EUKARYOTIC DNA METASE.

I- SIMILARITY: SOME TO BACTERIAL RESTRICTION SYSTEMS
                                                                                                                                    STRAIN-DOMESTICA; TISSUE-LIVER, MEDLINE; 92193689.
Lefevre F. la Bonnardiere C., "The porcine family of interfer
                                                                                                                                                                                                                  Sus scrota (Fig.).
Eukaryota; Metazoa; Chordata; Crar
Eukaryota; Metazoa; Chordata; Crar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methyltransferase.";
J. Biol. Chem. 271:31092-31097(1996)
                                                                                                 J. Interferon [2]
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "New 5' regions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2] REVISIONS TO N-TERMINUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                      DCQLSILLLLSCSVLDSFGELIPQ 25
                                                                                                                                                                                                                                                                                                                                                                                                    DCNVLLKLVMAGEVTNSLGQRLPQ 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 33.8; Conservative
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1229
1620
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Methyltransferase; DNA-binding.
CYS/ARG/LYS-RICH.
                                                                                                         family of interferon-omega: functional studies of five Res. 11:341-350(1991).
                                                                                                                                                                             TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.0%;
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e murine and h
MACROPHAGES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
MW; F737100AD043E709 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB
Pred. No. 51;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                   Craniata; Vertebrata; Mammalia;
                                                                                                                                                   Mege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                     Suidae;
                                                                                                                                                   D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bestor T.H.,
                                                                                                                                                                                                                                                                           update)
 IFN-ALPHA
                                        gene
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                                                                                                                        cloning, related c
                                                                                                                                                                                                                      Sus.
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                                      encoding
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r DNA (cytosine-5)-
 HAVE ANTIVIRAL
                                                                                                                        genes.";
                                        biologically
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RESULT 9
TDT_MOUSE
ID TOT_MOUSE
AC P09838;
DT 01-MAR-1989 (
DT 15-FEB-2000 (
DE DNA NUCLEOTID
DE (TERMINAL DEO
GNOTT OR TDT.
OS EUKARYOTA; Me
OC EUTHORIA; ROD
RN [1]
RA KOIWAI O., YO
RN MEDLINE; 8628
RA KOIWAI O., YO
RT TISOLATION AN
RY MEDLINE; 8628
RA KOIWAI O., YO
RT TISOLATION AN
RY MEDLINE; 9321
RI NUCLEIC ACIDA
RY SEQUENCE FROM
RC STRAIN-BALB/C
RX MEDLINE; 9321
RT CHARACTERIZAT
RX MEDLINE; 9601
RA ROUGEON F., DA
RA R
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Best Local
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                         Rougeon F., Doyen N.;
"The two isoforms of mouse differ in both the ability localization.";
                                                                                                                                                                                                                                                        STRAIN-BALB/C; TISSUE-THYMUS;
MEDLINE; 93219079.
Doyen N., Fanton D'Andon M., Bentolila L.A.,
                                                                                                                                                                                                                                                                                                                                                                          Koiwai O., Yokota T., Kageyama T., Hirose T., "Isolation and characterization of bovine and deoxynucleotidyltransferase cDNAs expressible Nucleic Acids Res. 14:5777-5792(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID DISULFID
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X57191; CAA40477.1;
EMBL; M28623; AAA31053.1;
HSSP; P01563; lITF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                      Bentolila L.A.,
                                                                                                                                                                                             "Differential splicing in mouse thymus g
terminal deoxynucleotidyl transferase.";
Nucleic Acids Res. 21:1187-1191(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 86286588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                 CHARACTERIZATION OF MEDLINE; 96016194.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00266; INTERFERONAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LSILLLLSCSVLDSFGELIPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00252; INTERFERON_A_B_D; 00143; interferon; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Metazoa;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Mouse).
Metazoa; Chordata; Craniata; Ver
Mentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
24
24
52
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                                                                                                           Fanton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Multigene 1
23 PO
189 IN
122 BY
162 BY
21433 MW; 8
                                                                                                                                                      ALTERNATIVE FORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.3%;
                                                                                                        D'Andon
                                           terminal to add N
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BY SIMILARITY.
BY SIMILARITY.
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Pred. No.
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POTENTIAL.
                                                                                                        Υ.
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                                                                                                           Nguyen
                                           deoxynucleotidyl transferase regions and subcellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529
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ae; Murinae;
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                                                                                                      T.Q.,
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as its content
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                                                                                                                                                                                                                                        Nguyen T.Q., Rougeon ates two forms of
                                                                                                                                                                                                                                                                                                                                                                                            , Yoshida S., Ara
d mouse terminal
e in mammalian ce
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                                                                                                           Martinez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 cells.";
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RESULT 10

FAD1_YEAST

ID FAD1_YEAST STANDARD; PRT; 306 AA.

AC P38913;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-2000 (Rel. 39, Last annotation update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE FAD SYNTHETASE (EC 2.7.7.2) (FMN ADENYLYLTRANSFERASE) (FAD PYROPHOSPHORYLASE) (FLAVIN ADENINE DINUCLEOTIDE SYNTHETASE).

GN FAD1 OR YDL045C ORD (FLAVIN ADENINE DINUCLEOTIDE SYNTHETASE).
 RR RR OCC GREET BRACE
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Matches 10
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modified and this statement is not removed. Usage by an
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: TEMPLATE-INDEPENDENT DNA POLYMERASE WHICH CATALYZES THE RANDOM ADDITION OF DEOXYNUCLEOSIDE 5'-TRIPHOSPHATE TO THE 3'END OF A DNA INITIATOR. ONE OF THE IN-VIVO FUNCTION OF THIS ENZYME IS THE ADDITION OF NUCLEOTIDES AT THE JUNCTION OF THIS ENZYME IS THE ADDITION OF RUCLEOTIDES AT THE JUNCTION (N REGION) OF REARRANGED IG HEAVY CHAIN AND T CELLS.

-I- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE + (DEOXY NUCLEOTIDE)(M) = N PYROPHOSPHATE + (DEOXYNUCLEOTIDE)(M+N).

-I- COFACTOR: REQUIRES MAGNESIUM.
-I- SUBCELLULAR LOCATION: NUCLEAR (TDT-S) OR CYTOPLASMIC (TDT-L).

-I- ALTERNATIVE PRODUCTS: TWO ISOFORMS; TDT-L/ARRED, AND TOT-S(MALL); ARE PRODUCED BY ALTERNATIVE SPLICING. THE TDT-S FORM IS THE MAJOR FORM. THE TWO FORMS DIFFER IN SUBCELLULAR LOCATION AND IN ACTIVITY AS THE LONG CYTOPLASMIC FORM CAN NOT ACT ON NECESTAL.
                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00522; DNA_POLYMERASE_X PFAM; PF00533; BRCT; 1. PFAM; PF00966; DNA_POLYMERASEX; 1.
SEQUENCE FROM N.A. STRAIN-W303-1A / DMEDLINE; 95098000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
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                                                                                                                                                                                                                                                                                                              374
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BL; X68670; CAA48634.1; -.
BL; X68670; CAA48634.1; -.
BL; X68670; DA3595.
BC; MGI:98659; DTI.
INTS; PR00869; DNAPOLX.
INTS; PR00871; DNAPOLXTDT.
INTS; PR00871; DNAPOLXTDT.
INTS; PR00871; DNAPOLXTDT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-X FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                             LLLSCSVLDSFGELIPOPSNE 29
                                                                                                                                                                                                                                                                                                            LLLYCDILESTFEKFKQPSRK 394
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482 501 MI
26 26 M
29 9 F
193 193 R
287 287 Q
309 309 E
367 367 D
441 444 DF
529 AA; 60179 MW;
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               / D273-10B
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M -> T (IN REF. 1).
F -> L (IN REF. 1).
R -> G (IN REF. 1).
Q -> K (IN REF. 1).
E -> Q (IN REF. 1).
D -> H (IN REF. 1).
D -> H CON REF. 1).
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Pred. No. 23;
3; Mismatches
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23;
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 529;
                                                                              Saccharomycetales
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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EMBL; Z71781; CAA96444.1; -.
EMBL; Z747093; CAA98604.1; -.
PIR; S47906; S47906.
SGD; L0000598; FAD1.
PFAM; PF01507; PAPS_reduct; 1.
PFAM; PF01507; PAPS_TEDUCT; 1.
Transferase; Nucleotidyltransferase; FASEQUENCE 306 AA; 35546 MW; 55BBB83C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1999 (Rel. 38, Last annotation update)
PULMONARY SURFACTANT-ASSOCIATED PROTEIN)
PROTEIN)
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                                                         "Transcription and mRNA stability regulate developmental and expression of rabbit surfactant protein B gene."; Am. J. Physiol. 268:L481-L490(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paulin L., Saren A.M., Laamaanen P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ da
-i- FUNCTION: ADENYLATES FAN TO FAD:
-i- CATALYTIC ACTIVITY: ATP + FMN - DIPHOSPHATE
                                                                                                                                                                                                     STRAIN-NEW ZEALAND WHITE; MEDLINE; 95208794.
                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and characterization associated protein-B (SP-B) in t
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SEQUENCE OF 1-34 FROM N.A.
                                                                                                                                                                        Margana
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                              iochem. Biophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: SOME, TO BACTERIAL SULFATE ADENYLATE TRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCQVLLLLYLSC
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                                                                                                                                                                     R.K., Boggaram V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 66. 8; Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                 160:325-332(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spencer T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55BBB830163A457F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  of the cDNA for the rabbit.";
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RESULT 12
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Best Local
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15-JUL-1998
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
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DISULFID
CARBOHYD
SEQUENCE FROM N.A. STRAIN-VC-16 / DSM MEDLINE; 98049343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
Gene 165
                                                             DNA POLYMERASE (EC 2.7.)
POL OR POLB OR AF0497.
Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
                                                                                                                                                     DPOL_ARCFU 029753;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Luzi P., Anceschi M., Strayer D.S.;
"The upstream region of the SP-B gene: intrinsic promoter activity
and glucocorticoid responsiveness related to a new DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M24901; AAA31466.1; -.
EMBL; U17106; AAA67934.1; -.
EMBL; S80649; AAD14335.1; -.
PIR; A32421; LNRBB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96096536.
Luzi P., Anceschi M., S.
"The upstream region of
                                                                                                                                                                                                                             252 QLYCGLYLRCSSYDSIGQVPP
                                                                                                                                                                                                                                                        4 QLSILLLLSCSVLDSFGELIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SUBCELLAULAR LOCATION: EXTRACELLULAR.
SUBCELLANEOUS: PULMONARY SUBREACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 165:285-290(1995).

FUNCTION: PULMONARY SURFACTANT ASSOCIATED PROTEINS PROMOTE
ALVEOLAR STABILITY BY LOWERING THE SURFACE TENSION AT THE AIR-
LIQUID INTERFACE IN THE PERIPHERAL AIR SPACES. SP-B INCREASES
THE COLLAPSE PRESSURE OF PALMITIC ACID TO NEARLY 70 MILLINEWTONS
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                 STANDARD;
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36, Last sequence update)
37, Last annotation updat
(2.7.7.7).
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261
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                                                             Archaeoglobales;
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B.
SAPOSINS-LIKE TYPE A.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
POTENTIAL.
MISSING (IN REF. 2).
R -> P (IN REF. 1).
C -> R (IN REF. 2).
ELHTPOLLSLLSRGWDARAICALGAC ->
AAHAPAAEPAYGGLGPRULPGPEGRV (IN REMAINS).
423047A69B12DCB5 CRC64;
                                                                                                                                                                                                                              272
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                                                            Archaeoglobaceae
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RESULT
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SYPB_SYNY3 STANDARD; PRT; 810 AA.
P74296;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last annotation update)
PHENYLALANYL-TRNA SYNTHITASE BETA CHAIN (EC 6
                  Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanaba A., Yamada M., Yasuda M., Tabata S., Yamada M., Yasuda M., Tabata S., Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions. F., DNA Res. 3:109-136(1996).

-I- CATALYTIC ACTIVITY: ATP + L-PHENYLALANINE + TRNA(PHE) = AMP + PYROPHOSPHATE + L-PHENYLALANIX-TRNA(PHE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 97061201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00136; DNA_DOL_B;
Transferase; DNA-directed
DNA-binding.
SEQUENCE 781 AA; 89850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRNA LIGASE BETA CHAIN) (PHERS). PHET OR SLL1553.
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-!- CATALYTIC ACTIVITY: N DEOXYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechocystis
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PROSITE; PS00116; DNA_POLYMERASE_B;
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AF0497; -.
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8; Conserv
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HSSP; P27002; 1PYS.
PFAM; PF01588; trNA_bind; 2.
Aminoacyl-trNa synthetase; Prosecution of the companion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGR8_HUMAN STANDARD,

MGR8_HUMAN STANDARD,

O00222; O15493;

O1-NOV-1997 (Rel. 35, Created)

O1-NOV-1997 (Rel. 35, Last sequence update)

15-FEB-2000 (Rel. 39, Last annotation updat

15-FEB-2000 (Rel. 39, East annotation updat)
  EMBL; U92459; AAB;
EMBL; U95025; AAB;
GCRDB; GCR_1889;
GCRDB; GCR_2604;
MIM; 601116; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE: 97446143.
MEDLINE: 97446143.
Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui The human metabotropic glutamate receptor 8 (GRM8) gene: a disproportionately large gene located at 7q31.3-q32.1.", Genomics 44:232-236(197).
Genomics 44:232-236(197).
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J
Rosteck P.R. Jr., Johnson B.G., Schbepp D.D., Belagaje
"Group III human metabotropic glutamate receptors 4, 7
molecular cloning, functional expression, and compariso
pharmacological properties in RGT cells.";
Brain Res. Mol. Brain Res. 53:88-97(1998).
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Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MICS 44:232-236(1997).
FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR TO MEDITATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
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98141892.
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e R.M.;
7 and 8:
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Multigene
SIGNAL
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F17634;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
FIBRINOGEN GAMMA CHAIN PRECURSOR.
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PFAM; PF01094; ANF_receptor; 1.
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                                                                                              Pastori R.L., Moskai
"Estrogen regulation
expression.";
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                                 SEQUENCE OF 1-58 FROM TISSUE=LIVER;
                                                                                             expression.
                                                                                                                                                                                                                    Xenopus laevis (African clawed froc
Eukaryota; Metazoa; Chordata; Crani
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                 MEDLINE;
                                                                              Biochemistry
                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 90241882.
                                                                                                                                                                                                     Batrachia;
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Shepard A.R., Moser D.R., Holland L.J.;
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Xenopus
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S
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Pred. No. 56;
7; Mismatches
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V (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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lpoidea; Pipidae;
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Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGREGATION.

AGGREGATION.

SUBBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

HISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P02679; 1FIC:
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
PFAM; PF00147; fibrinogen_C; 1.
Blood_coagulation; Glycoprotein; Calcium; Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J02894; AAA49709.1; -.
EMBL; M35548; AAA03247.1; -.
PIR; A32670; A32670.
HSSP; P02679; 1FIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOI. Celi. Endocrinol. 72:213-220(1990).
-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family
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9 LLLLQSLALLSSAFGNIIPNTDN 31
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                                                                                                                                                                                                                                                                                                        11; Conservative
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                                   2000, 22:32:11
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INTERCHAIN (WITH C-33') (BY SIMILARITY).

INTERCHAIN (WITH C-32') (BY SIMILARITY).

INTERCHAIN (WITH BETA) (BY SIMILARITY).

INTERCHAIN (WITH ALPHA) (BY SIMILARITY).

INTERCHAIN (WITH BETA) (BY SIMILARITY).

INTERCHAIN (WITH ALPHA) (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                 Score 44.5; D:
Pred. No. 31;
4; Mismatches
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: мау 9, 2000, 22:27:16; Search time 64.29 Seconds (without alignments)
26.447 Million cell updates/sec

Title: Perfect score: Sequence: US-09-104-340-3 147 1 MDCQLSILLLLSCS

MDCQLSILLLSCSVLDSFGELIPQPSNE 29

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : PIR_63:*
1: pir1:
2: pir2:
3: pir3:
4: pir4: pir1: *
pir2: *
pir3: *
pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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receptor tyrosine kinase Mek4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: A45583
R:Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse A;Reference number: A45583; MUID:92031278
A;Rocession: A45583
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-983 <SAJ>
A;Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω G	32	31
43	43	43	43	43.5	44	44	44	44	44	44	44.5	44.5	44.5	44.5
29.3	29.3	29.3	29.3	29.6	29.9	29.9	29.9	29.9	29.9	29.9	30.3	30.3	30.3	30.3
130	117	94	80	364	1537	482	411	191	157	111	1039	591	438	276
μ	N	N	Ν	N	2	N	N	ν	N	N	ν	ν	N	N
JL0079	T20888	B40506	A35572	T10174	JC4172	A70963	T04987	S69735	S58068	D72112	138401	T39195	A32670	S31504
Ig kappa chain pre	hypothetical prote	pRF2 protein - hum	seminalplasmin pre	hypothetical prote	DNA (cytosine-5-)-	hypothetical prote		hypothetical prote	probable olfactory	hypothetical prote	ATP-driven ion pum	probable amino aci	fibrinogen gamma c	H+/K+-exchanging A

ALIGNMENTS

Query Match 100.0%; Score 147; DB 2; Length 983; Best Local Similarity 100.0%; Pred. No. 1.2e-13; Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 MDCQLSILLLLSCSVLDSFGELIPQPSNE 29	RESULT 1 A38224 A38224 protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human C.Species: Homo sapiens (man) C.Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999 C.Accession: A38224; B38224 R.Wicks, I.P.; Wilkinson, D.; Salvaris, E.; Boyd, A.W. Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992 A; Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expre A; Reference number: A38224; MUID:92179233 A; Molecule type: mRNA A; Residues: 1-983 <avic' #status="" (asn)="" (covalent)="" (covalent)<="" (ncbip:86627)="" 21-39;810-860="" 91ycoprotein;="" <aviz'="" <kin'="" <mat'="" <sig'="" <tma'="" a;="" accession:="" atp;="" autophosphorylation:="" b38224="" backbone="" binding="" c;="" carbohydrate="" cell="" cross-references:="" domain:="" eph;="" experimental="" extracted="" f;1-20="" f;21-983="" f;232,337,391,404,493="" f;542-565="" f;619-885="" f;627-655="" f;632,337,391,404,493="" fibronectin="" from="" gb:m83941;="" hek="" homology="" iii="" kinase="" kinase,="" leukemia="" line="" lk63="" molecule="" ncbi="" nid:9183931;="" note:="" phosphoprotein;="" phosphotransferas="" pid:9183932="" pidn:aaa58633.1;="" pre-b-cell="" predicted="" product:="" protein="" protein-tyrosine="" receptor="" region:="" repea="" residues:="" reywords:="" sequence="" signal="" site:="" source:="" superfamily:="" th="" transmembrane="" type="" type:="" typesine=""></avic'>
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A;Gene: CMP
C;Superfamily: v
F;1-29/Domain: v
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                                                                                               C;Superfamily: von Willebrand factor type A repeat homology; E;1-29/Domain: signal sequence #status predicted <SIG> F;30-500/Product: cartilage matrix protein #status predicted <F;43-210/Domain: von Willebrand factor type A repeat homology F;231-266/Domain: EGF homology <EGF>
                                                                                                                                                                                                                    A;Cross-references: EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163179 C;Genetics:
                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-500 <ASZ>
                                                                                                                                                                                                                                                                                                                                                                                                        cartilage matrix protein precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 C;Accession: S66522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z35595; PIDN:CAA84634.1; GSPDB:GN00020; CESP:C01G6.3 A;Experimental source: clone C01G6
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A; Residues: 1-495 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C01G6.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC;Accession: T18835
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Eur. J. Bioche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Berks, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T18835
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Best Local S
Matches 16
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Best Local S
Matches 21
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       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                     zodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.;
J. Biochem. 236, 970-977, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
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     Similarity
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                                                                                 Willebrand
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Pred. No. 1.8e
1; Mismatches
                                                                             factor type A repeat homology <VWA2>
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No. 4.
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                     Length 500;
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hypothetical protein F26B6.11 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change C;Accession: T01135
                                                                          RESULT
T01135
                                                                                                                                                                                                                                                                                                           A;Cross references: GB:M68514; NID:g454809; PIDN:AAA48666.1; PID:g211447 A;Note: sequence extracted from NCBI backbone (NCBIN:62405, NCBIP:62411) C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin ty C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein-ty:619-885/Domain: protein kinase homology <KIN>F;627-635/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
B45583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Ayres, M.D.; Howard, S.C.; Kuzio, Virology 202, 586-605, 1994
A; Title: The complete DNA sequence A; Reference number: A72850; MUID:94
A; Accession: D72861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acorf-91 protein - C; Species: Autogram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor tyrosine kinase Cek4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: dsDNA virus C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999 C;Accession: D72861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Identification of a new eph-related A; Reference number: A45583; MUID:92031278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Sajjadi, F.G.; Pasquale, New Biol. 3, 769-778, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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A; Residues: 1-224 < AYR>
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A; Residues: 1-983 <SAJ>
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Best Local Similarity
Matches 10; Conserv
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Best Local :
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Autographa californica nuclear polyhedrosis virus, AcMNPV
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0; MUID:94303173
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                                                                                                                                                                                                                     Score 51; DB Pred. No. 16; 2; Mismatches
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30-Apr-1999

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C; Species: Caenorhab
C; Date: 15-Oct-1999
C; Accession: T28131
R; Berks, M.
                                                                                       submitted to the EMBL Data Library, A;Reference number: Z19237 A;Accession: T20204 A;Status: preliminary; translated fi A;Molecule type: DNA A;Residues: 1-399 <WILD
                                                                                                                                                                                              hypothetical protein C54C8.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T20204 R;Dobson, R.
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A;Introns: 358/3; 439/3; 502/3; 565/1; 646/3; 701/2
A;Note: F26B6.11
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A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
A;Reference number: Z14198
A;Accession: T01135
                                       A; Experimental source: C; Genetics:
                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: C; Genetics:
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A; Residues: 1-147 <WIL>
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A; Residues: 1-901 < ROU>
       A; Map
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                      Gene:
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Best Local Similarity
Matches 17; Conserv
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     position: 1
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les 9; Conserv
                    CESP: C54C8.4
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                                                        EMBL: Z83102; PIDN: CAB05466.1; GSPDB: GN00019; CESP: C54C8.4 se: clone C54C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL:Z49073; PIDN:CAA88891.1; GSPDB:GN00020; CESP:ZK970.7
se: clone ZK970
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Pred. No.
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Pred. No. 24;
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                                                                                                                                                                                   November 1996
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RESULT
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R;Kimura, H.; Takeda, T.; Tanak
Blochem. Blophys. Res. Commun.
A;Title: Expression of rat DNA
A;Reference number: JE0378
A;Accession: JE0378
                                                                                                                                                                     A;Molecule type: mRNĀ
A;Residues: 1-1622 <KIM>
A;Cross-references: DDBJ:AB012214
C;Keywords: methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                  DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - C;Species: Rattus norvegicus (Norway rat) C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: tryptophan synthase beta chain; tryptophan synthase F;30-422/Domain: tryptophan synthase beta chain homology <TRPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE000908; GB:AE000666; NID:g2622579; PIDN:AAB85951.1; PID:g262
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence
A;Molecule type: DNA
A;Residues: 1-429 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A69000; MUID:98037514 A;Accession: F69063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: F69063
R; Smith, D.R.; Douce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tryptophan synthase, beta subunit homolog - Methanobacterium thermoautotrophicum (str C;Species: Methanobacterium thermoautotrophicum C;Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                  A; Status: preliminary
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DCNVLLKLVMAGEVTNSLGQRLPQ
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hys. Res. Commun. 253, 4
                                                                           Conservative
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Pred. No. 1e+02;
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Pred.
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 1218
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495-501, 1998
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25;
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27;
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interferon alpha-1 precursor - pig
C;Species: Sus scrofa domestic (domestic pig)
C;Date: 22-Nov-1993 *sequence_revision 10-Nov-1995 *text_change 16-Jul-1999
C;Accession: S23709; I46589
R;Mege, D.; Lefevre, F.; Labonnardiere, C.
J. Interferon Res. 11, 341-350, 1991
A;Title: The porcine family of interferon-omega: cloning, structural analysis, A;Reference number: S23709; MUID:92193689
A;Accession: S23709;
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J. Interferon Res. 6, 349-360, 1986
A;Title: Molecular cloning and sequencing of a gene encoding A;Reference number: 146589; MUID:87035119
A;Accession: 146589
    DNA nucleotidylexotransferase (EC 2.7.7.31) - mouse
N;Alternate names: terminal addition enzyme; terminal deoxyribonucleotidyltransferase
C;Species: Mus musculius (house mouse)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 18-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein SPAC23C4.05c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38260
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A; Introns: 23/1
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A;Experimental source: strain 972h-; cosmid c23C4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Harris, D.; Squares, R.; Barrell, submitted to the EMBL Data Library, A; Reference number: 221782
A; Accession: T38260
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A; Residues: 1-189 < LEF>
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A; Residues: 1-189 <MEG>
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72.7%;
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Pred. No.
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September 1997
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02-Jun-1988 #text_change 18-Jun-1999
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Search completed: Job time: 4157 sec

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hypothetical protein Y53C12B.1 - Caenorhabditis elegans
(; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T27133
R; Kershaw, J: Lennard, N.
submitted to the EMBL Data Library, September 1997
A; Reference number: Z20316
A; Accession: T27133
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A;Residues: 1-25, /M', 27-98, 'F', 100-192, 'R', 194-286, 'Q', 288-308, 'E', 310-366, 'D', 368-44
A;Residues: 1-25, /M', 327-98, 'F', 100-192, 'R', 194-286, 'Q', 288-308, 'E', 310-366, 'D', 368-44
A;Cross-references: EMBL:X68670; NID:9287808; PIDN:CAA48634.1; PID:9287809
C;Superfamily: DNA nucleotidylexotransferase
C;Keywords: alternative splicing; magnesium; nucleotidyltransferase; nucleus
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A;A;Accession: S30235
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R;Koiwal, O.; Yokota, T.; Kageyama, T.; Hirose, T.
Nucleic Acids Res. 14, 5777-5792, 1986
A;Title: Isolation and characterization of bovine
A;Reference number: A93633; MUID:86286588
A;Accession: B23595
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A; Introns: 51/2
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A; Residues: 1-529 < KOI>
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A;Experimental source: clone Y53C12B
                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-793 <WIL>
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Best Local S
Matches 10
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/.
2: /cgn2_6/ptodata/.
3: /cgn2_6/ptodata/.
4: /cgn2_6/ptodata/.
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/cgn2_6/ptodata/2/iaa/5COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-167-919A-3
US-08-167-919A-3
US-08-167-919A-3
US-08-167-275-4
PCT-US95-07372-2
US-08-827-291A-2
US-08-827-291A-2
US-08-207-904-17
PCT-US95-07302-2
US-08-207-904-17
PCT-US95-07302-2
US-08-168-249A-18
US-08-142-249A-18
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Sequence 21, Appl
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Sequence 3, Appl
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US-08-167-919A-10
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Patent No.
                                                     TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                   SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acid
TYPE: amino acid
TOPOLOGY: 15
MOLECULE TYPE:
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	N	Sequence 1, 1	Sequence 14,		'n	2	Sequence 2, 2	29	29	4		Sequence 68,			Sequence 31,	Sequence 31,
;	Appli	ppli	Appl	Appl	ppli	Appli	ppli	Appl	, Appl	Appli	Appl	App1	Appl	App1	Appl	App1

ALIGNMENTS

APPLICATION NUMBER: US/08/167,919A FILING DATE: 18-APR-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: PK6841 (AU) FILING DATE: 21-UN-1991 PRIOR APPLICATION NUMBER: PK992 (AU) FILING DATE: 21-DEC-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/AU92/00294 FILING DATE: 12-DEC-1991 PRIOR APPLICATION DATA: PCT/AU92/00294 APPLICATION NUMBER: PCT/AU92/00294 APPLICATION NUMBER: 31,346 REGISTRATION NUMBER: 31,346 REGISTRATION NUMBER: 31,346 REGISTRATION NUMBER: 9159 TELECOMMUNICATION INFORMATION: TELEPAN: (516) 742-4343 TELEPAN: (516) 742-4343 GENERAL INFORMATION: APPLICANT: Simpson, Richard J. APPLICANT: Wicks, Ian APPLICANT: Wicks, Ian APPLICANT: Wicks, Ian APPLICANT: Withinson, David TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE TITLE OF INVENTION: AND USE THEREOF NUMBER OF SEQUENCES: 14 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS: STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: U.S.A. ZIP: 11530 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0 COUNTRY: U ZIP: 11530 10, Application US/08167919A 5. 5674691 Release #1.0, Version #1

983 amino acids linear

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                                                                                                                    Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, G
                                                                                                                                                    Sequence 21, Application US/08702367A Patent No. 5981246
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENTIN Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
                                                                                            APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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STREET: 1040
CITY: Thousand Oaks
STATE: California
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
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TOPOLOGY: 11r
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
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Pred. No. 2.2e-14;
D; Mismatches 0;
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Pred. No. 2.2e-14;
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-702-367A-21
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                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/715,106

FILING DATE: 18-SEP-1996

CLASSIFICATION: 4-35

PRIOR APPLICATION UMBER: 08/167,919

FILING DATE: 18-APR-1994

APPLICATION NUMBER: 08/167,919

FILING DATE: 18-APR-1994

APPLICATION NUMBER: PK6641 (AU)

FILING DATE: 21-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: DECOMO / AIT

APPLICATION DATA:

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Best Local Similarity 100.0%;
Matches 29; Conservative 0
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FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
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LENGTH: 983 amino acids
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MEDIUM TYPE: Floppy disk
                                                                PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 11530
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COMPUTER: II
                                                                                                             FILING DATE:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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MBER: PCT/AU92/00294
19-JUN-1992
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                                                                                                                                    PK9992 (AU)
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04681-21
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-715-106-10
RESULT
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PCT-US95-04681-21
                                                                                                                             Query Match
Best Local :
                                                                                                             Matches
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Best Local :
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                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: WINTER: ROBERT B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 18% CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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LENGTH: 983 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                               MDCQLSILLLLSCSVLDSFGELIPQPSNE 29
                                             MDCQLSILLLSCSVLDSFGELIPQPSNE 29
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1840 Dehavilland Drive
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(516) 742-4366
                                                                                                             Conservative
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100.0%; Pred. No. 2.2e-14;
htive 0; Mismatches 0;
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                                                                                                         Score 147; DB 4;
Pred. No. 2.2e-14;
); Mismatches 0;
                                                                                                                                       Length 983;
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US-08-162-809-16
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                                                                                                                                                                                              Sequence 16, Application US/08162809 Patent No. 5457048
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Best Local
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                                                                          GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS O
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ZHOU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/1 FILING DATE: 04-JAN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: WORDERRECT 5.1
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
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TITLE OF INVENTION:
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STRANDEDNESS: UNI
                                                   STREET:
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      COUNTRY:
                                    CITY: San Diego
                                                                    ADDRESSEE:
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California
: United States of America
                                                   4370 La Jolla
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                                            CAMPBELL AND FLORES
10 La Jolla Village Drive,
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52.48;
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                                                   Suite
                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                      Length 982;
                                                                                                               METHODS OF USE
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-162-809-16
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US-08-167-919A-2
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                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNUBER: PK6841 (AU)
FILLING DATE: 21-JUN-1991
PRIOR APPLICATION UNUBER: PK9992 (AU)
FILLING DATE: 12-DEC-1001
PRIOR APPLICATION UNUBER: PK9992 (AU)
PRIOR APPLICATION UNUBER: PK9992 (AU)
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Best Local Similarity
Matches 11; Conserva
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APPLICANT: BOYD, AI
APPLICANT: Simpson
APPLICANT: Wicks,
APPLICANT: Ward, LA
APPLICANT: Wilkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08167919A
Patent No. 5674691
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                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEPAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WILKINSON, DAVID
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
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MEDIUM TYPE: Floppy disk
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FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                          ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
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OPERATING SYSTEM: PC-DOS/MS-DOS
                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ward, Larry D.
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MBER: PCT/AU92/00294
19-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.7%; Score 51; 52.4%; Pred. No.
                                                                                                                                                                                                             US/08/167,919A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.0%; Score 47; Best Local Similarity 100.0%; Pred. No. Matches 9; Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (516) 742-43
TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: 18-APP-18
APPLICATION NUMBER: p
FILING DATE: 21-JUN-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                  APPLICATION NUMBER: PK99: FILING DATE: 12-DEC-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
                                                                                                                                                                  FILING DATE: 21-JUN-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE TITLE OF INVENTION: AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/01
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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Ward, Larry D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simpson, Richard J.
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1 SANS UR
NO: 2:
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                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
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                                                                                                                                                   PK9992 (AU)
                                                                                                                                                                                                                                   08/167,919
                                                                                                                                                                                                  PK6841 (AU)
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US-08-167-919A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
""" onservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                 TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LD NO.
LACTERISTICS:
LYPE: amino acid
STANDEDNESS: si-
TOPOLOGY:
'YECULF'
'YECULF'
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                              REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                               APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PK6841 (AU) FILING DATE: 21-JUN-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08
FILING DATE: 18-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ELIPQPSNE 29
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5. 5674691
               amino acid
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                             19 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simpson,
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single
                                                                                                                                                                           Frank
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100.0%; Pr
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0.26;
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; MOLECULE TYPE: protein US-08-167-919A-3
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Best Local Similarity
Watches 9; Conserve
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US-08-715-106-3
                                        TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 18-PLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                        FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992
FILING DATE: 12-DEC-1991
PRIOR APPLICATION UMBER: PCT/AU
PRIOR DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, FTANK S.
REGISTRATION NUMBER: 31,34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                     TELECOMMUNICATION INFORMATION: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                         TELEFAX:
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                            TOPOLOGY:
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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                                                                                                                                           2: (516) 742-4343
(516) 742-4366
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; Pred. No.
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Query Match
Best Local Similarity

32.0%; 100.0%;

Score 47; Pred. No.

DB 3; 0.37;

Length 19;

Matches

9

Conservative

Mismatches

Indels

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RESULT 13
PCT-US95-07372-12
; Sequence 12, Application PC/TUS9507372
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                                                                                                                                            Matches
                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATE: 03-NOV-1332
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
APPLICATION NUMBER: 13-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                          NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                               1 MDCQLSIL--LLLSCSVLDSFGELI 23
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Reff, Mitchell E.
Rastetter, William H.
Rastetter, William H.
RASTERIAN Therapeutic Application
RVENTION: Radiolabeled Antibodies
RVENTION: Differentiation Antigen
                                                                                                                                                                                                                                                                                128 amino acids
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Hanna, Nabil
                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BURNS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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                                                                                                                                                        30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             John E.
                                                                                                                                        Score 45; DB Pred. No. 6.7; Mismatches
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to Human B Lymphocyte Restricted
for the Treatment of B-Cell
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                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                 ş
                                                                                                                                                                                                         Sequence 2, Application US/08827291A Patent No. 5874243
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 30309-3430

ZIP: 30309-3430

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: TOWN PC-DOS/MS-DOS
                                                                 GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Sathe, Ganesh
TITLE OF INVENTION: NOVEL OLRCC15 RECEPTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Oklahoma Medical Research Foundation TITLE OF INVENTION: Calcium Binding Recombinant TITLE OF INVENTION: Antibody Against protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Georg
                                 STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 23...129
COUNTRY:
                                                                                                                                                                                                                                                                                                                           1 MDCQLSI--LLLLSCSVLDSFGELI 23
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1 MDFQVQIFSFLLISASVIMSRGQII 25
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                 PΑ
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Pred. No.
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9.7;
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

IBM Compatible

Diskette

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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08207904 Patent No. 5477002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tuttle, AnnMarie
APPLICANT: Crossland, Lyle I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 316 amino acid
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEP: CORRESS:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LAZZAr, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CGC
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOPPY DESCRIPTION
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/207,904
FILING DATE:
CLASSIFICATION: 800
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,291A
FILING DATE: 28 MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                             CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CLBA CLBA CAMPRET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                             ZIP: 10532
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CQLSILLLLSCSVLDSFGELI 23
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                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                 CIBA-GEIGY Corporation
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     CGC 1624
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Pred. No.
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. 27;
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                                                                                                                                                                                 ;; TYPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-207-904-2
Search completed: May Job time: 4149 sec
                                                                                                                  Matches
                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                             Local Similarity hes 9; Conserv
                                                                                       1 MDCQLSILLLLSCSV---LDSFGELIPQP 26
                                                                                                                 Conservative
            9
                                                                                                                               29.6%;
            22:26:00
                                                                                                                ; Score 43.5; D; Pred. No. 48; 5; Mismatches
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21:52:03 ; Search time 50.71 Seconds (without alignments)
13.546 Million cell updates/sec
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19-JUN-1992; AU0294.
21-JUN-1991; AU-006841.
12-DEC-1991; AU-009992.
(HALL-) HALL INST MEDICAL RES WA
BOYD AD, Simpson R, Ward LD,
WPI; 93-036373/04.
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therapy etc.

Claim 6; Fig 1; 58pp; English.

This sequence represets human eph/elk-like kinase (HEK). HEK is expressed in both pre-B cells and T cell lines and in a number of tumours of human origin, eg. lymphoid tumours LK63, Lila-1 and JM, and the epithelial tumour HeLa. This receptor-type thymidine kina (TK) and/or its ligands are useful as agents in modulation of the
                                                                                                                                          Receptor-type tyrosine kinase reactive with monoclonal antibody III-A4 - is EPH-ELK-like kinase, useful for phosphorylating proteins in modulating pre-B, B and T cell function, in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer; expression vector; extracellular domain; human; HEK; eph/elk-like; kinase; pre-B; cell; T; tumour; lymphoid; LK63; Lila-1; JM; epithelial; HeLa; receptor-type; thymidine kinase; TK; ligand; B;cellular response; growth; differentiation.
                                                                                                                                                                                                          P-PSDB; R31466.
                                                                                                                                                                                                                                                                                                                                                                  WO9300425-A.
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HEK polypeptide.
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232. .234
/note= "N-link glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
630
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'note= "N-link glycosylation"
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840. .
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779
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391. .:
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                                                                                                                                                                                                                                                                                                                                                                                                                        "ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "ATP binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                              "Putative autophosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Transmembrane domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "N-link glycosylation"
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R76700
R76699
R27705
R922705
W73315
W83428
W83431
W83431
W23596
W31950
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Opossum kidney PTH
Parathyroid hormon
Munc13-1 interacti
Rat Munc13-1. Scre
Human LYST1 longer
Human by protein a
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Minimum DB Maximum DB

seq

length: 0 length: 1000000

Minimum

Total number of hits satisfying chosen parameters:

188963 seqs,

23686106 residues

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Title: Perfect score:

US-09-104-340-3 147

MDCQLSILLLSCSVLDSFGELIPQPSNE

29

Sequence:

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protein

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9,

2000,

protein search, using sw model

Copyright

GenCore version 4.5 (c) 1993 - 2000 Comp

Compugen

Database

A_Geneseq_36:*

Pred. No.

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed.

derived by analysis of the total score distribution.

SUMMARIES

Post-processing: Minimum Listing

Match

45

summaries

Result No. Score 55 55 48.5 47.5 43 147 Query Match Length В R90690 P82937 P70626 W10241 W10342 W405187 W410519 W47519 W47519 W47519 W47519 W47519 W47519 W88376
W88380
W88380
W88380
W88380
R075711
R075710
R075720
R04031
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30-DEC-1998.
17-JUN-1998; E04016.
19-JUN-1997; EP-201863.
(ALKU ) AKZO NOBEL NV.
Aitken RJ, Grootenhuis AJ, V
WPI; 99-095361/08.
N-PSDB; X06779.
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17-JUN-1998; E04016.
19-JUN-1997; EP-201863.
(ALKU ) AKZO NOBEL NV.
Altken RJ, Grootenhuis AJ, Van D
WPI; 99-095561/08.
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This is a partial sequence of human sperm specific antigen 4.1. The sequence was deduced from a cDNA clone (see X06777) isolated from a human testicular cDNA ilbrary using marmoset 4.1 cDNA as probe. A full-length sequence for protein 4.1 is provided in 48380. Human and marmoset sperm proteins 4.1 and 6.7 (see W88373-80) and nucleotide sequences (see X06772-79) encoding them are new. The proteins are sperm specific and can be used in a contraceptive vaccine to prevent or reduce fertility in a subject without the autoimmune reactions that are a serious side-effect of without the autoimmune reactions that are a serious of vectors and
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W88378
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                                                                                                                                                                                                                                                                                              W88380 standard; Protein;
W88380;
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                                                                                                                                                                                                Homo sapiens.
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vaccine; contraceptive;
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No. 6.2e-14;
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0.88;
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DT 20
DE D6
ET D6
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Gallus sp.
W09515375-A.
08-JUN-1995.
07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RES FO Pasquale EB, Sajjadi FG;
WPI; 95-215256/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New sperm proteins 4.1 and 6.7 - useful as a contraceptive vaccine claim 8; Page 32-3; 44pp; English.

This is a full-length sequence of human sperm specific antigen 4.1 The sequence was deduced from a cDNA clone (see X06777) isolated from a human testicular cDNA library using marmoset 4.1 cDNA as probe. Human and marmoset sperm proteins 4.1 and 6.7 (see W88373-80) and nucleotide sequences (see X06772-79) encoding them are new. The proteins are sperm specific and can be used in a contraceptive vaccine to prevent or reduce fertility in a subject without the autoimmune reactions that are a serious side-effect of prior art female contraceptive vaccines. Expression vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 85-89; 129pp; English.

Probes derived from the EPH-related PTKS Cek4 (Q90659) and Ce (Q90660) were used to isolate novel CDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues and also in the adult brain and retina. Sequence 983 AA;
                                                                          Key
                                                   protein
                                                                                                 plasmid
                                                                                                                           Deduced
                                                                                                                                                20-DEC-1990
                                                                                                                                                                            R07640;
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Matches 13
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10-JUN-1988; US-204645.
20-APR-1989; US-341080.
(GEHO-) General Hospital Corp
Fisher RA, Schooley RT, Hirsch M
WPI; 90-007302/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R04031;
R04031;
29-MAY-1990 (first entry)
Full length T4 encoded by plasmid p170-2.
Soluble T4; p170-2; anti-retroviral agent
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.

Disclosure; Fig 1; 121pp; English.

Disclosure; Fig 1; 121pp; English.

Entire sequence from T4-encoding plasmid p170-2. It is almost identical to the sequence published by Maddon et al. (1985) with the exception of three codon changes. At T4 amino acid residue 3, (posn. 403 of entire sequence) Lys is encoded in stead of Asn. At posn. 64, (posn. 464) Arg replaces Trp and at posn. 231, (posn. 631) Ser replaces Phe.

Soluble T4 can be produced by truncating the CDS to remove the transmembrane and cytoplasmic domains. The soluble forms may be
                                                                                                                                             ARC and HIV infection.

Disclosure; fig 1; 100pp; English.

The sequence differs from that determined by PJ Madden et al., [Cell, 42 pp. 93-104 (1985)] in three places due to three nucleotide substitutions. The Asp reported at position 3 by Madden et al. was the result of a sequencing error [DR Littman et al. Cell, 55, p.541 (1988)].

X = stop codon.
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                 The sequence was deduced from the cDNA insert of p170-2. Soluble T4 constructs may be produced by truncating this sequence fragments from position 400 to 799, removing the transmembrane and intracytoplasmic domains whilst retaining the extracellular region responsible for HIV binding. The sol. T4 is combined with an anti-
                                                                                                                                                                                                                                                                                                           Combinations of soluble T4 protein and anti-retroviral agent having synergistic activity in treatment and prevention of A
                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; Q03005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 90-254040/33.
N-PSDB; Q05607.
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18-JAN-1990: U00358.
18-JAN-1989: US-300096.
(HARD) HARVARD COLLEGE.
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13; Conser
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653
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Pred. No. 95;
4; Mismatches
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149 4

QHCIILLSCHPQDAFLXLVSTQPSH

174

QLSILLLLSCSVLDSFGELI-PQPSN

28

Query Match Best Local Matches

Similarity

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frame of human immunomodulatory protein BL-1 encoding cDNA (given in CV 30915). The present invention describes a plasmid which comprises a concleotide sequence (NS) that encodes:(a) an immunomodulating protein concleotide sequence (NS) that encodes:(a) an immunomodulating protein concleotide sequence (NS) that encodes:(a) an immunomodulating protein concleotide from interleukin (IL)-12, granulocyte-macrophage colony stimulating factor (GN-CSF), IL-1, tumour necrosis factor (TNF)-alpha, concleotide from interleukin (IL)-12, granulocyte-macrophage colony concleotide for the present invention can be concleoted to regulatory elements. Products of the present invention can be used to induce an immune response to an antigen such as a pathogen conclinked to cells associated with autoimmune diseases or an allergen. They can be used for immunotherapy or to provide a protective immune conclined to cells associated with autoimmune diseases or an allergen. They can be used for treating subjects with an allergic reaction, pathogen infection, hyperproliferative disease concertive immune diseases e.g. rheumatoid conclined an allergic reaction, pathogen infection, hyperproliferative disease concertive immune diseases e.g. rheumatoid concertive multiple sclerosis, Sjogren's syndrome, sarcoidosis, insuling spondylitis, scleroderma, polymyositis, dermatomyositis, psoriasis, conditis, Grave's disease, autoimmune thyroiditis, ankylosing conditis, Grave's disease, autoimmune thyroiditis, asthma and concertive disease, autoimmune disease and ulcerative disease.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compositions for immuno-therapy and protection - comprise nucleotide sequences encoding an immuno-modulating protein and antigen, used for e.g. infections, cancer or auto-immune disease Example 6; Fig 14; 136pp; English.

The present sequence represents the protein from the third reaches.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APOL-) APOLLON INC.
(UYPE-) UNIV PENNSYLVANIA.
Bagarazzi ML, Boyer JD, Ki
WPI; 98-261495/23.
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23-OCT-1997; U19502.
23-OCT-1996; US-028613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunomodulatory protein BL-1 3.
Human; BL-1; immunotherapy; vaccine; immunomodulatory protein; HIV;
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03-NOV-1998.
19-MAY-1995; 444454.
02-OCT-1987; US-104461.
02-OCT-1982; US-355298.
01-NOV-1982; US-433128.
23-AUG-1991; US-43327.
11-SEP-1992; US-949327.
11-SEP-1992; US-444454.
   US5827694-A.
27-OCT-1998.
19-MAY-1995;
02-OCT-1987;
08-MAR-1982;
01-NOV-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 14A; 48pp; English.

This is the amino acid sequence of porcine interferon alpha-1, as deduced from the open reading frame of a cDNA clone (see V68167). The invention provides bovine, murine, porcine, feline, laprine and rat mature alpha, beta and gamma interferons and their propeptides (see W63895-905, W63918 and W70582-85). Recombinant DNA methods can be utilised to prepare these non-human animal interferons in amounts sufficient to enable the determination of their blochemical properties and bloactivities, and hence to allow efficient production for commercial or biological exploitation.

Interferons are useful as antiviral and antitumour agents.
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W83902;
15-FEB-1999 (fir
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Interferon-alpha 1; leukocyte interferon; virucide; antiviral;
                                                                                                                                                                                                                                                                                                                Peptide
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446171.
US-104461.
US-395298.
US-438128.
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                                                                                                                                                                                                       1. 23
/label= Sig_peptide
/label= Mat_protein
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/note- "
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24. .189
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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1; leukocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 189
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          interferon; virucide; antiviral;
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expressing human cytochrome p450 and a yeast NADPH-P450 reductase

PS Examples; Page 23-25; 124pp; English.

CC cDNA was amplified by PCR using the primers 087735-8. The product was

CC cloned into the yeast expression vectors pAAH5N or pAHRR to produce the

CC vectors p2C9 for the expression of the cytochrome P450 alone or p2C9R

CC for co-expression with the yeast NADPH-P450 reductase.

CC The vectors are used in a method for evaluating the safety of a chemical

CC compound by reacting the chemical compound with recombinantly produced

CC human cytochrome P450 molecular species and variants (087716) and

CC or 3A4 (087717), or their auxillary species and variants (087718-32), and

CC yeast NADPH-P450 reductase, either as a fused protein or in cell

CC extracts, and analysing the resulting metabolite to assess the safety of

Che chemical compound. The method is useful for determining whether and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of porcine interferon alpha-1, deduced from a cDNA (see V08184). The invention provides bovine, porcine, feline and rabbit mature interferons and their propeptides (see W7324-35). Recombinant DNA methods can be used to propeptides (see W7324-35). Recombinant DNA methods can be used to proper these non-human animal interferons in amounts sufficient to enable the determination of their blochemical properties and bloactivities, and hence to allow efficient production for commercial or blological exploitation. Interferons are useful as antiviral and antitumour agents. A replicable expression vehicle comprising claimed non-human animal interferon nucleic acid, a process for producing such an interferon, and a microorganism (especially Escherichia coli) or cell culture transfected with the nucleic acid are claimed.
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Best Local
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21-SEP-1992; US-949327.

19-MAY-1995; US-446171.

(GETH) GENENTECH INC.

Capon DJ, Goeddel DV;

WPI, 98-593994/50.
                                                                                                                                                                                                                                                       WPI; 95-116991/16.
N-PSDB; Q87715.
Evaluation of safety
                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1994; 111298.
20-JUL-1993; JP-201120.
21-JUL-1993; JP-180246.
30-JUL-1993; JP-208279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytochrome P450 molecular species 2C9 protein.
Human cytochrome P450; amplification; PCR; primer; expression vector;
yeast NADPH-P450 reductase; safety; fusion protein; metabolite;
carcinogen; mutagen; liver metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bioactivity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V08184.
                                                                                                                                                                                                                                                                                                                          Hayashi
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SUMITOMO CHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best I
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Best Local
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13-JUL-1994; 161551.
13-JUL-1994; JP-161551.
(SUMO) SUMITOMO CHEM CO LTD.
WPI; 96-136337/14.
N-PSDB; T17404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Pages 11-13; 13pp; Japanese In numans
The present sequence is the human derived cytochrome (HDC)
P450209, which was obtd. from a commercial cDNA library. Yeast
were transfected with an expression vector contg. the HDC cDNA,
cultured and then disrupted to give a microsomal fraction. The
HDC was purified from the fraction, and used to immunise and
sensitise a mammal. Blood was drawn from the mammal, and an
anti-HDC antibody isolated. The antibody obtd. recognises HDC
P450209, partic. at a serum dilution rate of 1:10000, and is
substantially without cross reaction to other HDC P450 spp. .
Sequence 490 AA;
                       05-MAR-1996.
15-JUL-1994;
20-JUL-1993;
30-JUL-1993;
                                                                                                                                                                                      11-007-1996 (LITEL ELLY)
Human cytochrome P450 molecular species 2C9 protein.
Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;
liver; yeast; expression vector; metabolite; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human derived cytochrome P4502C9.

Human derived cytochrome; P4502C9; commercial cDNA library; yeast; transfection; recombinant production; expression vector; mammal; immunisation; sensitisation; antibody; determination; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemical compound, or its carcinogenic or mutagenic Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody recognising human derived cytochrome P4502C9 - specific detection of cytochrome P450 species in humans Example 1; Pages 11-13; 13pp; Japanese.
                                                                                                                           J08056695-A.
                                                                                                                                                                              carcinogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
J08027196-A.
                                                                                                                                                                                                                                                                                                       11-OCT-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                         standard;
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13; Conser
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13; Conser
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JP-201120.
JP-208279.
JP-136053.
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38.2%;
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Pred. No. 43;
6; Mismatches
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Pred. No. 43;
6; Mismatches
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RESULT
W27850
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CC This is the amino acid sequence of the human cytochrome P450 molecular CC species 209 protein. The corresp. gene was amplified from a human liver CC to generate plasmid p209 for prodn. of the yeast expression vector pAAH5N CC to generate plasmid p209 for prodn. of the cytochrome only or into the vector pAHFR to generate the plasmid p209R for co-prodn. with the yeast CC NADH-P450 reductase. The sequence is placed under control of the yeast CC ADH gene promoter and terminator.

CC The vectors are used in a method for evaluating the safety of a cpd. by reacting the test cpd. with recombinantly produced human cytochrome P450 cmol. species 1A2 (728380), 209, 201 (728382), 3A4 (728383) or their compliants (728384-98) together with yeast NADH-P450 reductase (either as a coll and the resultant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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Claim 6; Pages 309-310; 989pp; English.

Claim 6; Pages 309-310; 989pp; English.

The present sequence represents a Staphylococcus aureus protein of unknown function. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequences to control the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect
                                                                                                                                                                                                                                                                                                                                           21-AUG-1997.
19-FEB-1997;
20-FEB-1996;
                                                                                                                                                                                                                                                 Black MT, Burnham MK, Hodgson JE,
pratt JM, Reichard RW, Rosenberg MPI: 97-42465/39.
N-PSDB; T83813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrom
                                                                                                                                                                                             aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a fused protein or as a cell extract) and analysing the resultant metabolite. The cpd. is considered "safe" if it is detoxified or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NADPH reductase to determine whether the analyte cpd. is detoxified or metabolised to a carcinogen
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WPI; 96-182311/19.
N-PSDB; T28381.
                                                                                                                                                                                                            Novel polypeptide(s) from to isolate antimicrobial c
                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxic shock syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolised to a carcinogenic Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rendered carcinogenic or "unsafe" if it is not detoxified
                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
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13; Conserv
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US-011888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus protein of unknown function.
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112
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                                                                                                                                                                                                                               Staphylococcus aureus strain WCUH29
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Pred. No. 43;
6; Mismatches
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M, Ward JM;
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RESULT
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ID 41568
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AC W4
AC W4
AC W4
KW M6
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J EP-81642.

D 07-JAN-1998.

PF 02-JUL-1997; 304821.

PF 02-JUL-1996; US-021243.

PA (ELIL) LILLY & CO ELI.

PI Belagale RM, Wu S;

DR WPZ; 98-054913/06.

DR N-PSDB; V04206-07.

Human metabotropic glutamate receptor protein - agonists and metabotropic glutamate receptor bear neurodegenerative disc
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12-NOV-1993; U10953.
13-NOV-1993; US-978891.
03-NOV-1993; US-149099.
(IDEC-) IDEC PHARM CORP.
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Staphylococcal 1
skin syndrome, a
sequence 114 1
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Treating B cell lymphoma with chimeric antibody - against CD20, causing rapid depletion of peripheral B cells, also new antibodies and hybridomas Disclosure; Fig 4; 101pp; English.

The sequence is the murine variable region light chain derived from murine anti-CD20 monoclonal antibody 2BS.

See also 065529-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reffme; WPI; 94
                                                                                                                                                                                                                                                                                                                                                                                      Metabotropic glutamate receptor; mGluR8; human; agonist; antagonist; neurodegenerative disease; antipsychotic; anticonvulsant; analgesic; anxiolytic; antidepressant; antiemetic; therapy.
                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
EP-816498-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R55214 standard; Protein; 128 R55214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human metabotropic glutamate receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W41568 standard; Protein; 908
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W09411026-A.
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B cell lymphoma chimeric antibody;
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MDFQVQIISFLLISASVIMSRGQIV 25
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ll; Conservative
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Pred. No.
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Pred. No. 9.6;
3; Mismatches
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CD20; peripheral blood cells;
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This protein comprises a novel human metabotropic glutamate receptor, designated mGluR8. Its amino acid sequence was deduced from cDNA clones isolated from a human foetal retina cDNA library.

The metabotropic glutamate receptors are linked to mutiple second messenger pathways. They function to modulate the presynaptic release of glutamate, and the postsynaptic sensitivity of the neuronal cell to glutamate excitation. Host cells transfected with especially RC7-18 host cells transfected with greynaptic sensitivity of the capacitally RC7-18 host cells transfected with pGT-hamGluR8, are claimed. They can be used in claimed methods for evaluating the effectiveness of a test compound for the treatment or prevention of a condition associated with a deficiency or excess of stimulation of the human mGluR8 receptor. mGluR8 agonists and antagonists can be used to treat neurodegenerative diseases, or as antipsychotic, antiemetic agents.

Sequence 908 AA;
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Matches 11
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                                     CQL--SILLLSCSVLDSFGELIPQPSNE 29
                                                                             Conservative
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Search completed: May 9, 2000, 21:52:05 Job time: 3757 sec

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Minimum
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Listing first 45 summaries
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HSSP; PU0523; 2PTK. PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00109; PROTEIN_KINASE_TYR; 1. PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.	OMAIN. BELONGS TO THE EPH FAMILY. L26099; AAA64464.1;	I- SIMILARI	1 IMMUNOGLOBULIN-LIKE C2-TYP	AND IN THE FOREBRAIN, KHOMBOMERES R3 AND R5 OF THE HINDBRAIN AND IN THE PRONEPHROS.	AGE: PRESENT TRANSIENTLY IN VISCERAL		TYROSINE PHOSPHATE!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN	N THE DIFFERENTIATION OF	-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY (BY		genes, has localized expression in a subset of neural crest and neural	T.D.;		EURAL	SEQUENCE FROM N.A.	ranopus.	ia; Anura; Mesobatrachia; Pipoidea; Pipidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;	ous labyis (African clawed	(PAGLIACCIO).	0	15 Last	(TrEMBLrel. 01, Created)		OIROA DEFITATANDO. DEM. DOS	JIT 1

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TYROSINE-PROTEIN KINASE
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PFAM; PF000041; fn3; 2.
PFAM; PF000069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
 SEQUENCE FROM N.A.
MEDLINE; 96125143.
XU Q., ALLDUS G., HOLDER
"Expression of truncated
                                                                                            Eukaryota;
Batrachia;
                                                                                                                        Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein
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                                                                             Xenopus.
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TIAADESETQVDIGDRIMKLNTEVRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL
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Mesobatrachia; Pipoidea; Pipidae;
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Sek-1 receptor
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FROTEIN KINASE.

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POSPHORYLATION (AUTO-) (POTENTIAL).

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9; Mismatches 32
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Matches 175
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NP_BIND
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CARBOHYD
SEQUENCE
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hindbrain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
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   267
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                                                                                                                                                                                                                                                                                                         cal Similarity
175; Conser
 EEHNGGCQ
                              EERGFMCQ
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16
548
570
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191
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745
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REAL STREET

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EMBL; x91191; CAA62601.1; -...
HSSP; P00523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROM; PF00041; fn3; 2.
PFAM; PF000536; SAM; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF014044 EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00109; TYRKINASE PRINTS; PR00014; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Development 121:4005-4016(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN. SIMILARITY: CONTAINS 2 FIBROMECTIN TYPE III-LIKE DOMAINS. SIMILARITY: TO OPHER PROTEIN-TYROSINE KINASES IN THE CATAL DOMAIN. BELONGS TO THE EPH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: '
DEVELOPMENTAL STAGE: E:
AT LOWER LEVELS IN R2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY OR MOVEMENT OF CELLS.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY). REQUIRED FOR INTERACTIONS IDENTITY OR MOVEMENT OF CELLS.
                                                                                                                                                                                                                                    PSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT
                                                                                         TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF
                      TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGY
                                                                       TIAADESFTQVDIGDRIMKLNTEVRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL
                                                                                                                                                                  NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID 144
TVRNLAQFPDTITGSDTSSLVEVRGSCVDNSEEKDVPKMYCGADGEWLVPIGNCLCNAGF
                                                                                                                                              DWIPRSGAQRVYVEIKFTLRDCNSLPGVMGTCKETFNLYYYESNNDKERFIRETQYVKID
                                                                                                                                                                                                                   PASEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMESSQNNWLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
bulin domain.
                                                                                                                                                                                                                                                                                        66.6%;
ilarity 70.6%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                    109840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXPRESSION OCCURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              otein kinase; i
Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                        Score 977; DE
Pred. No. 2.46
89; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
PHOSPHORYLATION OPPOTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTE
IG-LIKE C2-TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYS-RICH.
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYROSINE-PROTEIN KINASE RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                  028DBBDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Phosphorylation;
; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE
                                                                                                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S IN R3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S THAT REG
                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-A FAMILY
REGULATE T
                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŗ5
                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              986;
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                                   263
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 266
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Best Local Similarity

65.48;

4;

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PROSITE; PS00107; I
PROSITE; PS00109; I
PROSITE; PS00790; I
PROSITE; PS00791; I
PFAM; PF00041; fn3
DOMAIN
NP_BIND
NP_BIND
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                           DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peripheral nervous system.";
Mech. Dev. 68:173-177(1997).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phas:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
EPH-LIKE RECEPTOR TYROSINE KINASE PRECURSOR (EC 2)
                                                                                                                                                                                                                                                                      PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                             PRINTS; PRO0109; TYRKINASE. PRINTS; PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             042422
                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                    Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARAUJO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS
RESTRICTED TO PROSOMERES 1 AND 2 IN THE DIENCEPHALON AND ALL THE
RHOMEOMERES IN THE HINDBRAIN DURING SEGMENTATION STAGES. LATER ON,
A SUPERIMPOSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION
OF SEVERAL AXONAL TRACTS. IN THE SOMITIC MESODERM, THE EXPRESSION
CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST
AND MOTOR AXONS THROUGH THE SCLEROTOMES.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALLYTIC
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression of chick EphA7
                                                                                                                                                                                                                                                                                                                                                                       Y14271; CAA74643.1; -. P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M., NIETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98092111.
                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                   Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                     PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_TYR; 1.
RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
                         CEPHA7).
                                                                                                                                                                                                           Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phasianidae;
 ¥,
                                PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (
                                                                                                                                   CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE DOMAIN. CYS-RICH.
POTENTIAL.
1; 6B6BFD17
                                                                                                          FIBRONECTIN TYPE-III
                                                                                                                                                                                 EPH-LIKE RECEPTOR TYROSINE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                     kinase; ATP-binding; Phosphorylation; oprotein; Signal; Immunoglobulin domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; ianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          during
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78)
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                                  (POTENTIAL)
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                                                                                                          SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                               KINASE.
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Query

63.7%;

Score 934.5;

8

13;

Length

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RESULT
013146
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                             ZFIN; ZDB-GENE-990415-58; ZUAL.

R PROSITE; PS00107; PROTEIN_KINASE_TYP; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FALSE_NEG.

PRAM; PF00069; pkinase; 1.

PRAM; PF00069; SAM; 1.

DR PFAM; PF00044; EPH_Ibd; 1.

DR PFAM; PF00041; fn3; 2.

DR PFAM; PF00041; fn3; 2.

DR PRINTS; PR00109; TYRKINASE.

DR PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            013146;
               Transferase;
Receptor; Tr
                                                                                                                                                                                                                                                             ++
                                                                                                                                                                                                                                                                                                                                  developing zebrafish nervous system.
Dev. Dyn. 209:166-181(1997).
-!- FUNCTION: RECEPTOR FOR MEMBERS (
                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Buteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (Tremblrel. 04, 01-JUL-1997 (Tremblrel. 04, 01-NOV-1999 (Tremblrel. 12, EPH-LIKE KINASE 1 PRECURSOR
                                                                                                                                                                                                  ÷÷
                                                                                                                                                                                                                                                                                                                                                                                      BOVENKAMP D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                      <del>-</del>
                                                                                                                                                                                                                                                                                                 +
                                                                                                                                                                                                                                                                                                                                                             Novel Eph-family receptor tyrosine kinase working zebrafish nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                            DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                        SIMILARITY: TO OTHER DOMAIN. BELONGS TO THE
                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: TYPE TISSUE SPECIFICITY: WIDELY
                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                    TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                            SYSTEM
                                                                                                                                                                                                                                                                                                                           ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLSCSV----LDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCSAEGEWLVPIGKCICKAGYQQKGDTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMLCSVWLLRFAHTGE---AQAAKEVILLDSKAQQTELEWISSPPNGWEEISGLDENYTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGACIALVSVKVYYKKCWSIIENLAIFPDTVTGSEFSSLVEVRGTCVSSAEEEAENSPKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETDYDTGRNIRENQYVKIDTIAADESFTQGDLGERKMKLNTEVREIGPLSKKGFYLAFQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176;
                                                                                                                                                                                                                                                                                                                                                                                                 97329578
   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Immunoglobulin domai 20 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                          AAC60220.1;
2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                              z
                                                                                                                                                                                                                                                                                                                                                                                      GREER P.;
                                                                                                                                                                                                                                                                                                                         PATTERN
                                                                                                                                                                                                                                   PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                         FORMATION
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Last annotation update)
(EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
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3; Mismatches
                                                                                                                                                                                                                                                                                                A PROTEIN
                                                                                                                                                                                                                                                           I MEMBRANE
EXPRESSED I
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ches 41;
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                                                                                                                                                                                                                        R FAMILY.
                                                                                                                                                                                                                                                           E PROTEIN.
IN THE DEVELOPING ZEBRAFISH
                                                                                                                                                                                                                                                                                                                       EPHRIN-B FAMILY. MAY
N THE DEVELOPING NERVO
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Cypriniformes;
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                                                                                                                                                                                                                                   CATALYTIC
                                                                                                                                                                                                                                                                                                PROTEIN
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Best Loca
Matches
SEQUENCE FROM N.A.

COOKE J.E., XU Q., WILSON S.W., HOLDER N.;

Dev. Genes Evol. 206.515-531(1997).

EMBL; AJ005030; CAA06303.1; -.

HSSP; P00523; 2PTK.

ZEIN; ZDB-GENE-990415-61; rtk4.

PROSITE; PS00791; RECEPTOR TYR_KIN_V_2; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                          073879;
073879;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
EPH-LIKE RECEPTOR TYROSINE KINASE RTK4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
DISULFID
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
SEQUENCE
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DOMAIN
TRANSMEM
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                                                                                                                                                                 Submitted
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 Cyprinoidea; Cyprinidae;
                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                        Brachydanio
                                                                                                                                                                                    COOKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVCNVMEANQNNWLRTGLIQREGAQRVYVEIKFTLRDCNSLPGVPGTCKETFNVYYHESN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPPRMYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILVICQALRNY-----PDNEVTLLDSMSAPGDLGWEAYPSEGWEEISVMDERNIPMRTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADGGWLVPIGRCVCRPGFEEVDGHCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDHGV----KFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQD
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                                                                                                                                                                 (MAR-1998)
                                                                                                                                                                                                                                   o rerio (Zebrafish) (Zebra dar
Metazoa; Chordata; Craniata;
1; Teleosted; Euteleosted; Ost
a; Cyprinidae; Rasborinae; Dar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPH-LIKE KINASE 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 1.4e
14; Mismatches
                                                                                                                                                                EMBL/GenBank/DDBJ
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POTENTIAL.
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POTENTIAL.
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10D38182
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; Ostariophysi; C;
; Danio.
                                                                                                                                                                                                                                                                                    danio)
                                                                                                                                                                                                                                                                                                                                                                                                              088
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1.4e-71;
hes 57;
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Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

DR PFAM; PF001404; EPH_lbd; 1.

DR PFAM; PF000069; Pkinase; 1.

DR PFAM; PF00041; fn3; 2.

FT NON_TER 1

TT NON_TER 880

2 SEQUENCE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
Q91571
-!- SIMILARITY: CONTACT.

R EMBL; U14164; AAA74888.1; -.

R HSSP; P00523; 2PTK.

DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNIDER PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1
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Best Local S
Matches 149
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; I
Batrachia; /
                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TEMBLREL 12, EPHRIN TYPE-B RECEPTOR XEK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XEK.
                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 95215070.
                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91571;
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                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID BLASTULA TRANSITION AND REAPPEARS AT LATE NEUTULATION. EXPRESSED AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC STACES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBIQUITOUSLY EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION I THE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE RETINA OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EBHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVN
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149; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Last sequence update)
, Last annotation update)
PRECURSOR (EC 2.7.1.112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 838.5;
Pred. No. 2.1e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7C139606 CRC32;
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                                                                 UNKNOWN_1
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ies 33;
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Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                WILY. MAY PLAY A
L NERVOUS SYSTEM.
P + PROTEIN
                                                                                                                                                                                                                                                                                                                                                   receptor
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RESULT
OA 3477
ID AC OO
DT OO
DT OO
DT OO
DT OO
CO OC
CO OC
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Best Local Similarity
Matches 143; Conserv
                                                                                                                             043477 PRELIMINARY;
043477;
01-JUN-1998 (Tremblrel. 0
01-JUN-1998 (Tremblrel. 0
01-NOV-1999 (Tremblrel. 1
PROTEIN-TYROSINE KINASE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00790
PROSITE; PS00791
PFAM; PF00041; 1
PFAM; PF00069; 1
PFAM; PF000536; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
DISULFID
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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DOMAIN
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DOMAIN
DOMAIN
                                                                                    Homo sapier
Eukaryota;
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PFAM; PF00069; pkinase; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF01404; EPH_lbd; 1.

PRINTS; PR01109; TYRKINASE.

Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;

Transferase; Tyrosine-protein; Signal; Immunoglobulin domain
SEQUENCE FROM N.A.
SEDLINE; 96154673.
IKEGAKI N., TANG X.X.,
SULMAN E.P., BRODEUR G.
                                                                                                                      ЕРНВ2.
                                                                          Eutheria;
                                                                                                                                                                                                                                                                                  236
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                                                                       ryota; Metazoa; C
eria; Primates; C
                                                                                                                                                                                                                                                                            YLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.4%;
LIU.,
                                                                                                                                06, Created)
06, Last sequence update)
12, Last annotation updat
EPHB2V.
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 X.G., BIEGEL J
PLEASURE D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
CYS-RICH.
FIERONECTIN TYPE-III.
FIERONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLARION (AUTO-) (
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 768.5;
Pred. No. 8.9e
55; Mismatches
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.9e-64;
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               Α.,
                                                                                                                                              update)
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               ALLEN
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               c.,
                                                                                      Mammalia
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               YOSHIOKA
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RACSOLT
OCA 3369
ID 369
ID 370
OCA 360
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C 043569;

T 01-JUN-1998 (TrEMBLrel. 06, Created)

T 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

JT 01-JUN-1998 (TrEMBLrel. 12, Last annotation update)

DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

DE EPH-LIKE RECEPTOR TYROSINE KINASE HEPHB1C

(EPH-LIKE RECEPTOR TYROSINE KINASE HEPHB1D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim
Matches 138;
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SUBMITTED (SEP-1997) to the EMBL/GenBank/DI
EMBL; AF025304; AAB94602.1; -.
HSSP; P00523; 2PTK
HSSP; P00523; 2PTK
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROM; PF01404; EPH_1bd; 1.
PFAM; PF01404; EPH_1bd; 1.
PFAM; PF01404; EPH_1bd; 1.
PFAM; PF00109; PKINASE; 1.
PFAM; PF00053; SAM; 1.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
STEIN E., SCHOECKLMANN H.O., STEIN E., SCHOECKLMANN H.O., SUBMITTED TO THE EMBL; AF037333; AAB94628.1; -EMBL; AF037334; AAB94628.1; -HSSP; P08631; 2HCK.
PFAM; PF000041; fn3; 2.
PFAM; PF00069; pkinase; 2.
PFAM; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tyrosine-protein kinase. SEQUENCE 1055 AA; 117492
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                             Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wolecular characterization and chromosomal localization of DRT (EPHT3): a developmentally regulated human protein-tyrosine kinase yene of the EPH family ".

jum. Mol. Genet. 4:2033-2045(1995).
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                                                                                                                                                                                                                                                                                                                                                                      sapiens (Human).
ryota; Metazoa; Chordata; Craniata; Vertebrata;
eria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEAVENGTVCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVK----FREHQFTKID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIAADESFSQVDLGGRVMKINTEVRSFGPVSRSGFYLAFQDYGGCMSLIAVRVFYRKCPR
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55.0%;
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ne EMBL/GenBank/DDBJ
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                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                         DANIEL
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                                                                                                                                                                                                                                     H.O.
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Best Local S
Matches 138
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01-MAY-1999
01-NOV-1999
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PRINTS; PR00109; TYPEFIII.
PRINTS; PR00014; FNTYPEIII.
SEQUENCE 943 AA; 105291;
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPH-LIKE
                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                            7
                                                                                                                                                                                         7 ILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISTPSHGWEEISGVDEHYTPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            c-Jun Kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIR
                                                                        TYQVCNVFEPNQNNWLLTTFINRRGAHRIYSEMRFTVRDCSSLPNVPGSCKETFNLYYYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYME
TOSVIATKKSAFWSEAPYLKVDTIAADESFSQVDFRGRLMKVNTEVRSFGFLTRNGFY
                                                                                                                                                        LLLLLESAV------AAMEETLMDTRTATAELGWTANPASGWEEVSGYDENLNTIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGFVNKKGFYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLLLESAV-----AAMEETLMDTRTATAELGWTANPASGWEEVSGYDENLNTIR
                                   SDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-KIDNEY;
E., HUYNH-DO U., L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQDYGACMILLSVRVFFKKCPSIVQNFAVFPETMTGAESTSLVIARGTCIPNAEEVDVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDSVIATKKSAFWSEAPYLKVDTIAADESFSQVDFRGRLMKVNTEVRSFGPLTRNGFYLA
                                                                                                                                                                                                                                                                                                                                                                                                                    P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AF037331; AAD02030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138;
                                                                                                                                                                                                                                         il Similarity
138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primates;
                                                                                                                                                                                                                                                                                                                                                            Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 10, (TrEMBLrel. 12,
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Human).
etazoa; Chordata; Craniata; Vertebrata; Mammalia;
etazos; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          ÅΆ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNTYPEIII.
A; 105291 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYROSINE
                                                                                                                                                                                                                                                                                                                                        110041 MW;
                                                                                                                                                                                                                                                         50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Created)
0, Last sequence up
2, Last annotation |
E KINASE HEPHB1.
                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α.,
                                                                                                                                                                                                                                     Score 739.5; DB 4
Pred. No. 4.7e-61;
3; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 739.5; DB 4
Pred. No. 4.4e-61;
3; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                        DF5C8ED3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CERRETTI D.P., DANIEL r, EphB1/ELK, couples 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4C78A21 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               984
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                                                                                                                                                                                                                                                                          DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
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                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L T.O.;
ligand
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                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activation
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                     182
                                                                                                                 126
                                                                                                                                                        56
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RESULT
Q91735
      TACOCOCO SEETT TO THE TRANSPORT OF THE T
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                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF00069; pKinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Novel members of the eph receptor tyr during xenopus development.";
Oncogene 11:1745-1752(1995).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF 1
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91735
Q91735;
                                                                                                                                                                                                                                                                                               Receptor;
SIGNAL
  NP_BIND
DISULFID
BINDING
ACT_SITE
MOD_RES
                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TremBLrel. 01, Last sequence update)
01-NOV-1999 (TremBLrel. 12, Last annotation update)
EPHRIN TYPE-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 96068901. SCALES J.B., WINNI
                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASE
                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                        Transferase; Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0109; TYRKINASE.
PRINTS; PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN PRE-SOMITIC
MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST
ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER
IN INTESTINE, KIDNEY, OVIDUCT AND PHARXYX.
DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
SIMILARITY: TO OTHER PROTEIN TYROSING FANILY.
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQDVGACVALVSVRVYYKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQDYGACMILLSVRVFFKKCPSIVQNFAVFPETMTGAESTSLVIARGTCIPNAEEVDVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L43620; AAA93526.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR) (TCK)
                                                                                                                                                                                                                                                                                                                     Transmembrane;
    535
556
536
178
178
316
424
424
609
615
734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
    12,
                                                                                                                                                                                                                                                                                             otein kinase; ATP-binding; Phosphorylation
Glycoprotein; Signal; Immunoglobulin doma
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                   ATP (BY SIMILA
BY SIMILARITY.
ATP (BY SIMILA
BY SIMILARITY.
                                                                              PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                              FIBRONECTIN
                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                    EPHRIN TYPE-B RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                       CYS-RICH
  PHOSPHORYLATION
                                                                                                                                                                                         IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                         (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.S., SHEA L.J.,
tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        974
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                                                                                                                          TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPHRIN-B
(AUTO-) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SARGENT T.D.;
subfamily expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEVELS
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200

TGAESTSLVIARGTCIPNAEEVDVPIKLYCNGDGEWMVPIGRCTCKPGYEPENSVACK

257

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RESULT

1D 95143

1D 979

1AC 99

1AC 90

1AC 
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Best Local S
Matches 134
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             095143;
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY 1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOY-1999 (TrEMBLrel. 12, Last annotation update)
EPH-LIKE RECEPTOR TYROSINE KINASE HEPHBIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor; Kinase. SEQUENCE 973 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1997) to the EMBL/GenBa
EMBL; AF037332; AADD2031.1; -.
HSSP; P00523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-KIDNEY;
STEIN E., SCHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                               217
                                                                             140
                                                                                                                         157
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FTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVK----FREHQFTKIDTIAADESFTQMD
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(NOV-1997) to the
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Pred. No. 1.2e
51; Mismatches
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                             Score 713.5; DB 4;
Pred. No. 1.3e-58;
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v; BD419F6D CRC32;
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Best Local Similarity 50.4
Matches 122; Conservative
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HSSP; P00523; ZPTK.
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PROM; PF01404; EPH_1bd; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF00556; SAM; 1.
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Q07494;
01-NOV-1996
01-NOV-1999
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    Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniat;
Neognathae; Galliformes; Phasianidae;
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SAJJADI F.G., PAS(
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MEDLINE; 93288
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VTSELAWTTHPETGWEEVSGYDEAMNPIRTYQVCNVREANQNNWLRTKFIQRQDVQRVYV
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  gallus (Chicken)
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RECEPTOR_TYR_KIN_V_2;
PROTEIN_KINASE_TYR; 1
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Pred. No. 2.2e-55;
1; Mismatches 57
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Best Local Sim
Matches 112;
Mech. Dev. 48:153-164(1994).

EMBL; U11493; AAA67925.1; -.

HSSP; P00523; 2PTK.

MGD; MGI:104770; Ephb3.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; h
Neognathae;
[1]
                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                        Q60669 PRELIMINARY;
Q60669;
Q1-NOV-1996 (TIEMBLTel. 01,
Q1-NOV-1996 (TIEMBLTel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE, 93288394.
SAJJADI F.G., PASQUALE E.B.;
"Five novel avian Eph-related
expressed.";
                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 95200798.
                                                                                                                                                                                                                                                                                                                                                     EPHB3 OR ETK2.
                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12, PROTEIN KINASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 8:1807-1813(1993).
EMBL; Z19110; CAA79526.1; -.
                                                                                                                                                                                                             RUIZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                    Identification of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
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Local Similarity
                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQKIYYELKFTLRDCNSIPLYLGTCKETFNLYYMESDDDHGVK----FREHQFTKIDTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMDTRTATAELGWTANPPSGWEEVSGYDENLNTIRTYQVCNVFEPNQNNWLLTTFINRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00536;
PF00069;
PF01404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENNVACR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADESFSQVDFGGRLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADESFTOMDLGDRILKLNTEIREVGPVNKKGFYLAFODVGACVALVSVRVYFKKCPFTVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AHRIYTEMRETVRDCSSLPNVPGSCKETFNLYYYETDSVIATKKSAFWTEAPYLKVDTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERGFMCQ
                                                                                                                                            Dev. 48:153-164(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     952
                                                                                                                                                                                                         CONLON F.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
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; pkinase; 1.
; EPH_lbd; 1.
; fn3; 2.
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Pred. No. 1.8e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                      kinases
                                                                                                                                                                                                         .J.;
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hes 53;
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Mus.
                                                                                                                                                                                      the
                                                                                                                                                                                    myocardium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
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Best Local Similarity
Matches 108; Conser
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PFAM; PFO
PFAM; PFO
NON_TER
SEQUENCE
             EMBL; L43
HSSP; P00
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PRAM; PF0
PFAM; PF0
PFAM; PF0
PFAM; PF0
                                                                                                                                  --- SUBCELLULAR COCATION: TYPE I MEMBRANE PROTEIN.
--- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN THE BRAIN ,
SPINAL CORD AND IN THE FIRST AND FOURTH VISCERAL ARCHES. ;
ABUNDANT IN ADULT BRAIN, WITH LOWER LEVELS IN EXE, HEART,
OVIDUCT, LUNG AND PHARYINX.
--- IDEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
--- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATAL
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
--- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
--- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update
EPH RECEPTOR TYROSINE KINASE (XELE) (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipida
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 96068901.
SCALES J.B., WINNING R.S., RENAUD C
SCALES J.B., WINNING R.S., RENAUD C
"Novel members of the eph receptor
during Xenopus development.";
Oncogene 11:1745-1752(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91736;
Q91736;
                                                                                                                                                                                                                                                                   -I- CATALYTIC ÁCTIVITY: ATP + A PROTEIN TYROSINE -
TYROSINE PHOSPHATE.
 Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus.
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          SITE: PS00107; PROTEIN_KINASE_ATP; 1.
SITE: PS00109; PROTEIN_KINASE_TYR; 1.
SITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
SITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
M; PF00041; fn3; 2.
M; PF00041; fn3; 2.
M; PF00059; pkinase; 1.
M; PF000536; SAN; 1.
M; PF000536; SAN; 1.
                                                                                                                                                                                                                                                                                             SIMILARITY).
                                                                                                                                                                                                                                                                                                         FUNCTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACIANAVEVSVPLKLYCNGDGEWMVPVGACTCATGHE 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRG
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PF000536;
PF00069;
                                                                                                                 L43621; AAA93527.1; P00523; 2PTK.
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Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPH_lbd;
fn3; 2.
SAM; 1.
pkinase;
1
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8 %
8 %
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                                                                                                                                                                                                                                                                                                        MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 589; DB
Pred. No. 5.8e
45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
 kinase;
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                                                                                                                                                                                                                                                                                                                                           C.S., SHEA L.J.,
tyrosine kinase
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ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata;
ea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
.8e-47;
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                                                                                                                                                                                                                                                                                                        EPHRIN-B
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                                                                                                                                                                                                                                                                                                                                           SARGENT T. subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                        FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                      Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    938;
                                                                                                                                                                                                                                                                                PROTEIN
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Search completed: May 9,
Job time: 2380 sec
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Best Local Similarity 55.1
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor;
NON_TER
DOMAIN
TRANSMEM
DOMAIN
CORRECT
STE
MOD_RES
CARBOHYD
CARBO
                                                                                                                   182 HVVCK 186
                                                                                                                                                                                                             267 GFMCQ 271
                                                                                                                                                                                                                                                                                                                                                               150
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                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                                          RVYVEMRFTVRDCSSLPNVPGSCKETFNLYYYETDSNIDNKISTFWNESPYLKVDTIAAD 61
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662
696
252
344
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398
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                      2000, 22:31:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE.

ATP (BY SIMILARITY).

BY SIMILARITY.

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (POTENTIAL).

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

C096D006 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 563.5; DB 13; Length 902;
Pred. No. 1.4e-44;
2; Mismatches 34; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN (BY SIMILARITY).

CYS-RICH.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: May 9, 2000, 22:32:11; Search time 49.21 Seconds (without alignments) 167.716 Million cell updates/sec

Title: Perfect score: Sequence: US-09-104-340-4 1466

1 MDCQLSILLLLSCSVLDSFG......VPIGKCSCNAGYEERGFMCQ 271

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 83857 segs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

333334 433210	28 2 2 2 3 2 3 2 3 2 3 3 3 3 3 3 3 3 3 3	Result
528.5 510 492 99.5 90	1466 1400.5 1399 1399 1002 995 995 995 995 995.5 925.5 925.5 925.5 772 772 772 773 760.5 752.5 698.5	Score
000401	100 95.5 95.5 89.5 68.4 67.5 67.5 67.2 63.2 63.2 51.3 51.3 51.3 51.3 51.3 51.3 51.3 51.3	Query Match
1006 1006 987 987 982 3110	983 983 983 984 948 1035 986 1037 1037 1037 1037 986 988 998 988 998 988 998 988 998 998	gth
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P21709 homo sapien O15197 homo sapien P54761 mus musculu P54760 homo sapien O63852 sarcophyton P24043 homo sapien	P29320 homo sapien P29319 mus musculu O08680 rattus norv P29318 gallus gall P54758 rattus norv O62413 mus musculu Q07496 gallus gall P54764 homo sapien Q61772 mus musculu P54755 gallus gall Q51772 mus musculu P54759 rattus norv P54759 rattus norv P54759 rattus norv O61772 mus musculu P54759 rattus norv O9127 mus musculu P54759 rattus norv O90127 mus musculu P28693 gallus gall P29323 homo sapien P54763 mus musculu P28694 coturnix co O03145 mus musculu P54764 homo sapien P547674 mus musculu P54754 mus musculu	Description

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5.5	5.5	5. 5	5.6	5.6	5.6	5:6	5.7	5.8	5.8	6.0
806	897	406	1376	1029	1098	461	788	380	3106	1376
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SYL_HELPJ	SAP1_YEAST	NPRA_BACST	VGL2_CVMJC	YFC5_YEAST	TSL1_YEAST	HMCS_ARATH	ITB3_HUMAN	I132_HUMAN	LMA2_MOUSE	VGL2_CVM4
	P39955 saccharomy	P43130 bac	Q02385 muri			P54873 arabidopsis			-	P22432 murine corc

ALIGNMENTS

DR	DR DR		88	នន	88	388	388	38	38	388	38	88	38	R.	R	R K	RX	RP	RE	잠:	RA	R 7	RN	88	SO	G E	E	3 5	Di d	38	RESULT	
PS50011; PROTEIN_KINASE_DOM;	014; F 109; T 0107; 0109;	HSSP; P00223; 2PTK. HSSP; P0523; 2PTK. MIM; 179611; -	an email to license@isb-sib.cl	Jsage by and for commerc	use by non-profit institutions as long as its content is in no way	and the EMBL outstatic	This correct Door other is constituted to the Life Life LOWALING.	DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.	-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC	I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +	FUNCTION.	ION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAI	J. Biol. Chem. 267:3262-3267(1992).	and	Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A., Welch K., Loudovaris M., Rockman S., Busmanis I.;	2147681.	SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.	Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).	man lymj	P., Wilkinson D., Salvaris E., Boyd A.W.;	MEDLINE; 92179233.	FROM N. A.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates: Catarrhini: Hominidae: Homo	`		EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.1112) (TYROSINE-PROTEIN	24, Last	(Rel. 24,	EPAGEHUMAN STANDARD; PRT; 983 AA.	LT 1	

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DOMAIN
                   Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Entheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC
KINASE RECEPTOR ETK1) (MEK4).
EPHA3 OR ETK1 OR MEK4 OR TYRO4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00790; RECEPTOR_TYR_KIN_
PROSITE; PS00791; RECEPTOR_TYR_KIN_
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PFAM; PF00041; fn3; 2.
                                                                                                                        EPA3_MOUSE P29319;
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  STRAIN-ICR
           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                           MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE
                                                                                                                                                                                                RMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                      LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP
                                                                                                                                                                                                                                                                                                          HYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETF
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                                                                                                                                                                                                                           LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP
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                                                                                                                                   STANDARD;
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RECEPTOR_TYR_KIN_V_2;
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                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

POTENTIAL.

Y -> L (IN CAA01906).

V -> L (IN CAA01906).

V -> L (IN CAA01906).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
TISSUE-EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                          0;
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CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHRIN TYPE-A RECEPTOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                  Score 1466;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kinase; ATP-binding; Phosphorylation;
pprotein; Signal.
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                               ion update)
(EC 2.7.1.112)
                                                                                                    update)
                                                                                                                                                                                                      271
                                                                                                                                  983
                                                                                                                                  Å
                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
1.1e-122;
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                                                                                (TYROSINE-PROTEIN
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R PRINTS; PRO0104; ENTEPEIII.

R PRINTS; PR00109; TYRKINASE_ATP; 1.

R PROSITE; PS00107; PROTEIN_KINASE_TTR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

R PRAM; PP00041; fn3; 2.

R PRAM; PP00069; pkinase; 1.

R PRAM; PP000536; SAM; 1.

R PRAM; PP00536; SAM; 1.

R PRAM; PP01404; EPH_1bd; 1.

R PRAM; PP01404; EPH_1bd; 1.

R PRAM; PF01404; EPH_1bd; 1.

R PRAM; PP01404; EPH
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SEQUENCE
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HSSP; P16109;
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Sajjadí F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M68513; AAA39521.1; -.
EMBL; M68515; AAA39522.1; ALT_SEQ.
PIR; A45583; A45583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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TISSUE SPECIFICITY: GREATEST LEVELS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES
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                                95.5%;
95.9%;
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                                                                                                                                                 MW;
Score 1400.5; DE Pred. No. 2e-116; 3; Mismatches
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POTENTIAL.
POTENTIAL.
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ATP (BY
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                                                                                                                                                                           MISSING
                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III.
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A6655D8107A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A LIY.Y. MOTHER A.M.;

A LIY.Y. MOTHER A.M.;

TIL-1 beta alters the expression of the receptor tyrosine kinase

T **T-EphA3 in neonatal rat cardiomyocytes.";

L Am. J. Physiol. 274:H331-H341(1998).

C -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS

C -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS

C -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

PROTEIN TYROSINE PHOSPHATE.

C -!- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -!- SIMILARITY: TO OPHER PROTEIN-TYROSINE KINASES IN THE CATALYT

C -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
PRINTS; PRO0014; ENTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.

PFAM; PF00041; fn3; 2.

PFAM; PF000505; SAM; 1.

PFAM; PF000505; SAM; 1.

PFAM; PF001104; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPA3_RAT STANDARD; PRT; 008680; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence u 15-FEB-2000 (Rel. 39, Last annotation EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EKINASE RECEPTOR REK4).
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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HSSP; P16109;
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Sciurognathi; Murida
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annotation
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2.7.1.112)
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ae; Murinae;
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Best Local S
Matches 258
SEQUENCE FROM N.A.

MEDLINE; 9203178.

Saljadi F.G., Pasquale E.B., Subramani S.;

"Identification of a new eph-related receptor tyre
from mouse and chicken that is developmentally re-
at least two forms of the receptor.";

New Biol. 3:769-778(1991).

-IPHRIN-A2, -A3, -A4 AND -A5.

EPHRIN-A2, -A3, -A4 AND -A5.

-ICATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
PROTEIN TYROSINE PHOSPHATE.
                                                                                                         P29318;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence updat
01-NOV-1997 (Rel. 35, Last annotation upd
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.
KINASE RECEPTOR ETK1) (CEK4).
EPHA3 OR ETK1 OR CEK4.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; V
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SIGNAL
CHAIN
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DOMAIN
NP_BIND
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Receptor; Transmembrane;
                                                                                                    Neognathae;
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                                                                                                   Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                 lata; Craniata; Vertebrata;
Phasianidae; Phasianinae;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred. No. 2.7e
3; Mismatches
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V; F170C49312F7A0AB
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           TYROSINE
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?.7e-116;
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                          EPHRIN-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AUTO-) (BY SIMILARITY).
                                                tyrosine kinase
y regulated and e
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                          (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                          FAMILY.
                                                                                                  ; Archosauria; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                           984;
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                                                 e gene
encodes
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                         Aves;
                                                                                                                                                                                                                                                                                          180
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Best Local
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                             NP_BIND
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics in the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal.

SIGNAL 1 19 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M68514; AAA48666.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
   188
                         189
                                                 128
                                                                     129
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                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE I TISSUE SPECIFICITY: GREATEST BRAIN.
SIMILARITY: TO OTHER PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; PF00041; fn3; 2.

; PF00069; pkinase; 1.

; PF00536; SAM; 1.

; PF01404; EPH_lbd; 1.
в45583; в45583.
                                                                                                       QVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESD
                                                         DDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGA
                                                                                            QESNVMDHSQNNWLRTNWIPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESD
                                                                                                                                        LLLLCAALGSAGRLSARPGNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTY
                                             P00523:
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2PTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                     89.3%;
91.6%;
                                                                                                                                                                                                                                              109910
                                                                                                                                                                                                                                              ₩.
                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
                                                                                                                                                                                      8
                                                                                                                                                                                                Score 1309;
Pred. No. 2
                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                   ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORELATION (AUTO-) (BY SIMILARITY).

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                               EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                            POTENTIAL.
; E8895F0BDF77651E CRC64;
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEMBRANE PROTEIN.
LEVELS OF EXPRESSION OCCURRING IN
                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                .6e-1
                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                             B
                                                                                                                                                                                                          Length
                                                                                                                                                                                      Indels
                                                                                                                                                                                     0,
                                                                                                                                                                                    Gaps
                                                                    188
 247
                                              187
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Best Local S
Matches 180
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PRINTS; PR00014; FNTYPEIII.

PRINTS; PR00109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00701; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                              DOMAIN
NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P54758;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.1:
KINASE RECEPTOR EHK-2) (EPH HOMOLOGY KINASE-2)
EPHA6 OR EHK2 OR EHK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Maisonpierre P.C., Barrezueta N.X., Yancopoult
"Ehk-1 and Ehk-2: two novel members of the Eph
kinase family with distinctive structures and
Oncogene_8:3277-3288(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATI-
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A
-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; MEDLINE; 94067777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPA6_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249
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                          EEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLV
DAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKETLRDCNSIPWV
                                                                                     CEVREFLL-----QFGFFLPLLTAWTGDCSHVSNQVVLLDTSTVMGELGWKTYPLNGW
                                                                                                                           CQLSILLLLSCSVLDSFGELIP------QPSNEVNLLDSKTIQGELGWISYPSHGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF01404;
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                            409
948
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; pkinase; 1.
4; EPH_lbd; 1.
Tyrosine-protein
                                                                                                                                                                                                                                                                                A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                    948
549
943
943
7962
4096
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                                                                                                                                                                                             68.4%;
                                                                                                                                                                                                                                                                                  106235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
A47DC78EDB2DEF30 CRC64;
                                                                                                                                                                                             Score 1003;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271
                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPHRIN TYPE-A RECEPTOR 6. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kinase; ATP-binding; Phosphorylation;
pprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yancopoulos G.D.;
of the Eph receptor-like tyrosine
ctures and neuronal expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           948
                                                                                                                                                                                             DB 1;
3.3e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN.
KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .112)
                                                                                                                                                                                                                Length
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
                                                                                                                                                                                                                   948;
                                                                                                                                                                         18;
                                                                                                                                                                       Gaps
                                         112
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RESULT EPA6_M AC Q62413 DT Q1-NOV DT Q1-NOV DT Q1-NOV DT CEPHAG CO EUGHAT EUGHA
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                                                                                                                                          PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00186; EGF_2; UNKNOWN_1.

PFAM; PF00041; fn3; 2.

PFAM; PF00069; pkinase; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF01404; EPH_Lbd; 1.

Transferase; Tyrosine-protein kinase; ATP-1

Transferase; Tyrosine-protein kinase; ATP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWI
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the Euro
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Q62413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee A.M., Navaratham D., Ichimiya S., Greene M.I., Davis J.G.;
"Cloning of m-ehk2 from the murine inner ear, an eph family re-
tyrosine kinase expressed in the developing and adult cochiea.

DNA Cell Biol. 15:817-825(1996)

-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINI
EPHRIN-A1, -A2, -A3, -A4 AND -A5.

-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U58332; AAB53836.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KINASE RECEPTOR EHK-2) (EPH HOMOLOGY KINASE-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:108034; EPHA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 97047913.
Lee A.M., Navaratr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPHA6 OR EHK2 OR EHK-2.
                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATI
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSSEERDTPKLYCGADGDWLVPLGRCICTTGYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Glycoprotein; Signal.

1 22 POTENTIAL.
23 1035 EPHRIN TYPE-A RECEPTOR 6.
23 549 EXTRACELLULAR (POTENTIAL).
550 570 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
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                                                                                                                                             ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270
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                                                                                                                                             Phosphorylation;
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Best Loc
Matches
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Q1-NOV-1997 (Rel. 35, Cr

Q1-NOV-1997 (Rel. 35, La

Q1-NOV-1997 (Rel. 35, La

EPHRIN TYPE-A RECEPTOR 4

KINASE RECEPTOR CEK8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                  Oncogene 8:1807-1813(1993).
                                                                                        expressed
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neognathae; Galliformes; Phasianidae; Phasianinae;
                         <del>-</del>
                                            -
                                                                                                              Sajjadi F.G.,
                                                                                                                                               SEQUENCE
                                                                                                                                                                                                     Ando
                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-SPINAL CORL
                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                     EPHA4 OR CEK8.
                                                                                                                          MEDLINE;
                                                                                                                                    TISSUE-EMBRYO;
                                                                                                 "Five novel avian
                                                                                                                                                                                                                                                                                                                                                                                                                                       237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAI
EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHR
CAPALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADI
PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE!
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN
                                                                                                                                                                              receptor tyrosine kinase,
ypes of motoneurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEVREFLL-----QFGFFLPLLTAWTGDCSHVSNQVVLLDTTTVMGELGWKTYPLNGW
                                                                                                                                                                                                                                                                                                                                                                                CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                      KSAEERDTPKLYCGADGDWLVPLGRCICSTGYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKFTLRDCNSIPWV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIERKGFYLAFQDIGACIALVSVRVFYKKCPFTVRSLAMFPDTIPRVDSSSLVEVRGSCV
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                                                                                                                       93288394.
                                                                                                                                              OF 138-986
                                                                                                                                                                                                  Tanaka H.;
                                                                                                                                                                                                              Nakamura
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630
636
797
797
342
396
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                                                                                                 Fasquale E.B.;
/ian Eph-related
                                                                                                                                                                                                                                    CORD;
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą
                                                                                                                                                                                                            M., Hirokawa
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943
644
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396
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65.7%;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                          PRECURSOR
                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1002; DB 1;
Pred. No. 4.6e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                  tyrosine kinases
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                        Cek8,
                                                                                                                                                                                                             ;
;
                                                                                                                                                                             spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                          S OF THE EPHRIN-A FAMILY.
MORE POORLY TO EPHRIN-A2
ROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560B264194A5EF74
                                                                                                                                                                                                                                                                                                                         (E)
                                                                                                                                                                                                             Tanaka S.,
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                                                                                                                                                                                                                                                                                                                                                                               986
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C 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                              cord
                                                                                                                                                                                        transiently
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                                                                                                  are differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDRILKLNTEIREVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                  ; Archosauria;
Gallus.
                                                                                                                                                                                        expressed
                                                                                                                                                                                                            Α.,
 DOMAINS.
THE CATALYTIC
                                                                                                                                                                                                            Suda
                                                       AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                     A-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56
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Query Match
Best Local S
Matches 179
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS001186; EGF_2; UNKNOWN_1.
PROSITE; PS0014; fn3; 2.
PFAM; PF000536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                              NP_BIND
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D38174;
EMBL; Z19059;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
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DOMAIN
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entitles requires a license agreement (S. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
 267
                            264
                                                         207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                            NWVPRNSAQKIYVELKETLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID
                                                                                                                                                                                                                                              PSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT
                                                                                                                                                                       DWIPREGAQRVYIEIKFTLRDCNSLPGVMGTCKETFNLYYYESNNDKERFIRESQFAKID
                                                                                                                                                                                                                                 PANEVILLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRT
                            EERGFMCQ 271
                                                       TVRNLAQFPDTITGADTSSLVEVRGSCVNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGY
                                                                                    TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGY
EERNGECQ
                                                                                                                                                                                                                                                                                          179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF01404;
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                             20 986
20 547
548 559
570 986
532
27 635
3 746
3 779
3 408
408
138 R
109482 MW;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; BAA07373.1; -.
; CAA79509.1; -.
; 2PTK.
   274
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                                                                                                                                                                                                                                                                                                      68.1%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPHRIN TYPE-A RECEPTOR 4.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (BY SIN
FIBRONECTIN TYPE-III (BY SIN
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                       Score 998; DE
Pred. No. 9.7e
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase; ATP-binding; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                              -> G (IN REF. 2).
-> T (IN REF. 2).
BD88C2A5BD840A0F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
                                                                                                                                                                                                                                                                                                     DB 1;
.7e-81;
                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                               CRC64;
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SIMILARITY).
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commercial
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DE EPHRIN

DE EPHA4

OS ELCHAI

OC ELCHAI

RR FOX 61

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                          DOMAIN
DOMAIN
NP_BIND
BINDING
BINDING
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                               Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0014; ENTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROM; PF00041; fn3; 2.

PFAM; PF00040; pkinase; 1.

PFAM; PF00040; EPH_1bd; 1.

PFAM; PF01404; EPH_1bd; 1.

PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNCOGENE 10:897-905(1995).

- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
- EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2
- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
- PROTEIN TYROSINE PHOSPHATE.
- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN
- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CA-
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112
KINASE RECEPTOR SEK) (RECEPTOR PROTEIN-TYROSINE
EPHA4 OR SEK OR HEK8.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-tyrosine kinases.
Oncogene 10:897-905(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L36645;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95206782
Fox G.M., Holst P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA cloning and tissue distribution of five human protein-tyrosine kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R., Welcher A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602188;
                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holst P.L.,
                             N.A.
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2PTK.
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       109859
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                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
       ¥.
                                              ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (BY
FIBRONECTIN TYPE-III (BY
                                                                                                                                                                                                                                                                                                           EPHRIN TYPE-A RECEPTOR 4. EXTRACELLULAR (POTENTIAL). POTENTIAL.
    POTENTIAL.

1; 0C39C1152EDDD46F CRC64;
                                                                                                                                                                                                                  PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
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                                                                                                                                                                                                                     KINASE
                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KINASE HEK8).
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- ADP +
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THE CATALYTIC
                                                                                                                                                                                                                                           SIMILARITY).
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A-3.
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Best Local 9
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  EMBL; U07357; AAA17038.1; -.
HSSP; P00523; 2PTK.
MGD; MG1:99654; EPHA5.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1
                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (BRAIN-SPECIFIC KINASE)
                                                                                                                                                                                                                                                                                   Zhou R., Copeland T.D., Kromer L.F., Schulz N.T.; "Isolation and characterization of Bsk, a growth fac tyrosine kinase associated with the limbic system."; J. Neurosci. Res. 37:129-143(1994).
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BALB/C; TIS MEDLINE; 94194581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
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                                                                                                                                                                                                                                                                                                                             MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPA5_MOUSE
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                                                                                                                                                                                 EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: BRAIN.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA

DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                      FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLSC--SVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIR 66
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                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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68.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 995;
'```. 1.'
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                                                                                                                                                                                                                                                                                                       factor
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                                                                                                                                                                                                                                                                                                                                                                       Mus.
                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
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                                                                                                                                          restrictions
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for
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in no way
commercial
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EPA5_RA
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Best Local Sim
Matches 174;
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PROSITE; PS00791; RECEPTOR_1
PROSITE; PS01186; EGF_2; UNF
PFAM; PF00041; fn3; 1.
PFAM; PF00059; Pkinase; 1.
PFAM; PF000546; SAM; 1.
PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
SEQUENCE
                     Oncogene
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                        RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
SIGNAL
          SEQUENCE FROM
                                                                                                SEQUENCE
                                                                                                                  Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase;
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                                                                                                                                                                                                                                                                                EWLVPIGKCMCKAGYEEKNGTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                               FROM N.A.
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27
27
413
434
305
514
514
539
266
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           N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
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877
412
433
877
399
775
528
639
639
                                                                                                                              Chordata;
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TISSUE=BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN_1
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BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 990; DB
Pred. No. 4.3e
44; Mismatches
                                                                                                                                                                                                                                                                                305
                                                                                                                                                                                                                                                                                                      271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPHRIN TYPE-A
                                                                                                                  Craniata; Ve
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Si
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PBAS_RAT STANDARD: PRT; 1005 AA. PS4757; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1). EPHAS OR EKH1 OR EHK-1.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
MEDLLNE; 94067777.
Maisonpierre P.C., Barrezueta N.X., Yancopoulos G.D.;
Maison Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression.";
Oncogene 8:3277-3288(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCNYMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHGVKEREHQETKIDTIAADESETQMDLGDRILKLNTEIREVGPVNKKGEYLAFQDVGAC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL).
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54AD2DC864178214 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990; DB 1;
No. 4.3e-80;
                                                                                                                                                                  Vertebrata;
ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ignal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR 5. (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                  (TYROSINE-PROTEIN
                                                                                                                                                                  Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PRINTS; PRODO14; ENTYPEIII.

PRINTS; PROD109; PROTEIN_KINASE_ATP; FALSE_NEG.

R PROSITE; PSO0109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00779; RECEPTOR_TYR_KIN_V_1; 1.

R PROSITE; PS007791; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS001186; EGF_2; UNKNOWN_1.
     CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X78689;
HSSP; P00523;
PRINTS; PR0001
                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                    NP_BIND
                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                            ACT_SITE CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                        PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression and developmental regulation of Ehk-1, a neuronal Elk-like receptor tyrosine kinase in brain.";
Neuroscience 63:163-178(1994).
                                                                                        VARSPLIC
                                                                                                                                        VARSPLIC
                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                              Transferase;
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                                                                                                                                                               VARSPLIC
                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                        PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95206467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H., Steck A.J
                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
      170
566
578
669
979
                                                                                                                                                                                                                                    576
597
677
683
709
802
266
301
                                                                                        597
                                                                                                                                                                                                                                                                                                                                                                              Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Alternative splicing
                                                                                                                                       358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAA55357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        pkinase;
EPH_lbd;
                                                                                                                                                                                    1005
575
596
1005
938
691
709
802
266
425
438
438
      170
566
578
708
979
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TFEIEAVNGVSDLSPGTRQTVSVNVTTNQAA ->
SPLICED FORMS).

SGSCCECGCGGRASSLCAVAHPSLIW -> R (IN
SPLICED FORMS).

D -> E (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
T -> I (IN REF. 2).
T -> I (IN REF. 2).
                                                                                                                                                                                                                                                          PROTEIN KINASE.
ATP (BY SIMILAR:
ATP (BY SIMILAR:
BY SIMILARITY.
POTENTIAL.
                                                                                                        SPLICED FUKMS).
VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCYCEKDYFR
RESDPFTMACTR -> G (IN SPLICED FORMS).
RPPSAPRNAISNVNETSVFLEWIPPAOTGGGKDVSYYILCK
KCNSHAGYCEECGGHVRYLPQQIGLKNTSVMMADPLAHTNY
TPPTFAVMGYSDLSPGTRQYVSVNVTINQAA -> T (IN
                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
                                                                                                                                                                         POTENTIAL.
GRRRTQGRGGG -> DADGPRAQASWCHARR
SPLICED FORMS).
                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                          EPHRIN TYPE-A RECEPTOR 5
                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       noved. Usage by and for commercial (See http://www.1sb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breitschopf H.,
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RESULT 11
EPA5_HUMAN
ID EPA5_H
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Best Local Sim
Matches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         P54756;

D1-OCT-1996 (Rel. 34, Created)

O1-OCT-1996 (Rel. 34, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN-
KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-
TYROSINE KINASE HEK7).
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                        "cDNA cloning and tissue distribution protein-tyrosine kinases."; Oncogene 10.897-905(1995).
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                           MEDLINE; 95206782
Fox G.M., Holst P
                                                                                                                                                                                                                                                                                                                                                           Miescher
                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BRAIN;
                                                                                                                                                                                                                                                               Basu R., Welcher A.A.;
                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 25-1037
                                                                                                                                                                                                                                                                                                                                       Miescher G.C.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPHA5 OR EHK1 OR HEK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                          EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED ***

SYSTEM.
                                                             SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATADOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                           SYSTEM.
SIMILARITY: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EWLVPIGKCSCNAGYEERGFMCQ
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                                                                                                                                                                                                                                                                             Holst P.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                 FROM N.A
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 institutions as long
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Pred.
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as its content
                                                                                                                                                                                                                                                                           R.A., Janssen A.M.,
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                                                                                                                                                                                                                                                   human
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                                                                                                                                                                                                           FAMILY. BINDS
                                                                                                                                                                                                                                                 EPH-like receptor
                                                                                                                  IN THE NERVOUS
                                                                                         CATALYTIC
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not removed

noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/

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RESULT 12
EPA4_MOUSE
ID EPA4_M
AC Q03137
DT 01-OCT
DT 01-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 173
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.
          EPA4_MOUSE
Q03137;
Q1-OCT-1994
Q1-OCT-1994
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TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
BINDING
CARBOHYD
CARBOHY
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PFAM;
PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X95425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not rentities requires a license agreemen or send an email to license@isb-sib-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
                                                                                                                                                                              281
                                                                                                                                                                                                                  249
                                                                                                                                                                                                                                                           221
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                                                                                                                                                                                                     EWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                    QNGRNIKENQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVGAC
                                                                                                                                                                                                                                                                                                                                                          DHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGFVNKKGFYLAFQDVGAC
                                                                                                                                                                                                                                                                                                                                                                                                                  VCKVMEQNQNNWILTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD
                                                                                                                                                                                                                                                                                                                                                                                                                                         VCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ
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PF00069;
PF00536;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF01404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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          (Rel.
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; AAA74245.1; -.
; 2PTK.
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pkinase;
SAM; 1.
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be agreement (See
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MW;
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

POTENTIAL.

POTENTIAL.
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Pred. No. 1.8e
44; Mismatches
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Receptor;
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HSSP; P00523; Zrin.

HSSP; P00523; Zrin.

R PRINTS; PR00014; PNTYPEIII.

R PRINTS; PR00109; TYRKINASE.

JR PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

DR PRAM; PF000401; PAINASE; 1.

DR PFAM; PF000536; SAM; 1.

DR PFAM; PF001404; EPH_lbd; 1.

Transferase; Tyrosine-protein kinase; ATP

Transferase; Tyrosine-protein kinase; ATP
  EPHA4 OR SEK.

Mus musculus (Mouse).

Eukaryota; Metazoa; C

Eutheria; Rodentia; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X65138;
EMBL; X57241;
EMBL; S57168;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gilardi-Hebenstreit P., Ni
Chestier A., Wilkinson D.G
Oncogene 8:1103-1103(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "An Eph-related receptor protein t expressed in the developing mouse Oncogene 7:2499-2506(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last annotation EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (ECKINASE RECEPTOR SEK) (MPK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=C57BL; TISS MEDLINE; 93096484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilardi-Hebenstreit P., N
Chestier A., Wilkinson D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HINDBRAIN PATTERN FORMATION.

-I CAPALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = AI PROTEIN TYROSINE = AI PROTEIN TYROSINE = AI PROTEIN TYROSINE = BIOSPHATE.

-I SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I ALTERNATIVE PRODUCTS: A SHORTER FORM WITH A DELEGAMINO ACIDS: ALTERING THE CATALYTIC SITE MAY BE GIVEN ALTERNATIVE SPLICING.

ALTERNATIVE SPLICING.

-I TISSUE SPECIFICITY: HIGHEST LEVELS IN THE BRAIN, IN THE HEART, LUNG AND KIDNEY. IT IS SEGMENTALLY IN THE EMBRYONIC BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on if
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2
EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2
EPHRIN-A1, -A5. BINDS MORE POORLY TO EPHRIN-A2
EPHRIN-A
EPHRIN-
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TISSUE=EMBRYONIC
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nieto M.A., Frain M., Matto
D.G., Charnay P.;
r protein tyrosine kinase g.
ping mouse hindbrain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nieto
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.
        POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III (BY SIMILARITY).

FIBRONECTIN TYPE-III (BY SIMILARITY).
                                                                                                  EPHRIN TYPE-A
EXTRACELLULAR
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Charnay P.;
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C 2.7.1.112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
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ae; Murinae;
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K
                                                                                                RECEPTOR 4. (POTENTIAL).
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THE CATALYTIC
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Best Loc
Matches
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01-OCT-1996 (Rel. 34, L:
01-NOV-1997 (Rel. 35, L:
EPHRIN TYPE-A RECEPTOR:
KINASE RECEPTOR CEK7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        EPA5_CHICK P54755;
                                                                                                                                                                   MEDIINE; 95047429.
Slever D.A., Verderame M.F.;
"Identification of a complete Cek7 receptor protein coding sequence and CDNAs of alternatively spliced t Gene 148:219-226(1994).
-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A F
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                              EPHA5 OR CEK7.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phas;
                                                                                                                                                                                                                                                                                                                                                                                                                 CHICK
                                                                                                                                                                                                                                              TISSUE-BODY WALL;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                         EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATF + A PROTEIN TYROSINE - ADF + PROTEIN TYROSINE - PROPERTION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALDOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF
||||||||:::||||::||||
TIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PANEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMEASQNNWLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DWITREGAQRVYIEIKFTLRDCNSLPGVMGTCKETFNLYYYESDNDKERFIRESQFGKTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                        (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 35, Last annotation updat
-A RECEPTOR 5 PRECURSOR (EC 2.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              627
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                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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653
7746
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340
408
423
832
832
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                                                                                                                                                                                                                                                                              data; Craniata; Vertebrata;
Phasianidae; Phasianinae; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN SHORT ISOFORM)
V; D16AD8B85668C80E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    1013
                                                                                                                                                                                                                                                                                                                                       update)
2.7.1.112)
There are no rest
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.8e-79;
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                                                                                                                                                                                                                                                                                                                                        (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                      FAMILY.
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                                                                                                                                                                                                                                                                               Gallus.
                                                                                   CATALYTIC
                                                                                                                                                                      BINDS
                                                                                                          ВУ
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                                                                                                                                                                                                         kinase
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NR HSSP; PUOUS; ZFIN.

NR PRINTS; PRO0014; FNTYPEIII.

NR PROSITE; PRO0019; TYRKINASE_ATP; 1.

DR PROSITE; PSO01107; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS000119; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS000119; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS000790; RECEPTOR_TYR_KIN_V_1; 1.

DR PROSITE; PS000791; RECEPTOR_TYR_KIN_V_2; 1.

DR PROSITE; PS001186; EGEF_2; UNKNOWN_1.

DR PRAM; PF00041; fn3; 2.

DR PFAM; PF00069; pkinase; 1.

DR PFAM; PF00069; pkinase; 1.

DR PFAM; PF00136; SAM; 1.

DR PFAM; PF01404; EPH_1bd; 1.

KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;

KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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Best Local S
Matches 170
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DOMAIN
TRANSMEM
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CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
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BINDING
ACT_SITE
CARBOHYD
CARBOHYD
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EMBL;
HSSP;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U03910;
EMBL; U03910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                               137
 257
                                  249
                                                                       197
                                                                                                           190
                                                                                                                                                                                   130
                                                                                                                                                                                                                   77
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                                                                                                                                                                                                                LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ
                                                                                                                                          EWLVPIGKCLCKAGYEEKNNTCQ
                  EWLVPIGKCSCNAGYEERGEMCQ
                                                                                        VALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG
                                                                      TALVSVRVYYKKCPSVIRNLARFPDTITGADSSQLLEVSGVCVNHSVTDEAPKMHCSAEG
                                                                                                                                                                                                                                                                                                                                                                   170;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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AAB60614.1; -.
AAB60612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.6%;
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112245 MW;
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POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
SCCDHGCGWASSLRAVAYPSLIW
1 AND ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                               Score 947; DE
Pred. No. 3.4e
37; Mismatches
                                  271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC36FD6AEBF38382 CRC64;
                                                                                                                                                                                                                                                                                                                                                               DB 1; 1
3.4e-76;
nes 52;
                                                                                                                                                                                                                                                                                                                                                                                                Length 1013;
                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                   136
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RESULT 14
EPA7_HUMAN
ID EPA7_HUMAN
AC Q15375;
DT 01-NOV-1997

STANDARD;

PRT;

866

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(Rel. 35, Created)

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Query Match
Best Local S
Matches 171
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EPHA7 OR EHK3 OR HEK11.
                                                                                         BINDING
ACT_SITE
MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                        PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00791; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE: PS01186; EGF_2; UNKNOWN_1.
PFAM; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- EUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BI
EPHRIN-A1, "A2, "A3, "A4 AND "A5.
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATE
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                 CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                 PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-tyrosine kinases.";
Oncogene 10:897-905(1995).
                                                                                                                                                                                                                                                                                     PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0014
PRINTS; PR00109
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L36642; AAA74243.1; -. HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FOX G.M., Holst P.L., Chute H.T., Lindberg R.A., Jar Basu R., Welcher A.A.;

"CDNA cloning and tissue distribution of five human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            NP_BIND
                                                                                                                                                         DOMAIN
                                                                                                                                                                      DOMAIN
                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                            Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  PF00041; fn3; 2.
PF00069; pkinase; 1.
PF00536; SAM; 1.
PF01404; EPH_lbd; 1.
     171;
                Similarity
                                                                                                                                                                                                                                                            Transmembrane;
                                                                                         Tyrosine-protein
                                                                 A,
                                                                                                                                                                                                                                                                                                                                                                                                                TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                             FNTYPEIII.
                                                                                          998
556
577
998
438
943
6647
6647
758
758
                                                                 112096
             68.4%;
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Last annotation update)
R 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN)
(EPH HOMOLOGY KINASE-3) (RECEPTOR PROTEIN-
                                                                                                                                                                                                                                             Glycoprotein;
POTENTIAL.
                                                                 ¥:
  39;
 Score 927.5; D
Pred. No. 1.8e-
9; Mismatches
                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                 ATP
ATP
BY S
                                                                                        PHOSPHORYLATION (AUTO-)
POTENTIAL.
                                                                             POTENTIAL
                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                EPHRIN TYPE-A RECEPTOR 7.
                                                                                                                                                                                                                                                                     kinase; ATP-binding;
                                                                                                                 SIMILARITY
                                                                                                                          TEIN KINASE.
(BY SIMILARITY).
(BY SIMILARITY).
                                                                479B9CA0D2BB06EB
                                                                                                                                                                                                                                                         Signal.
                         DB 1;
                                                              CRC64;
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 Indels
                         Length
                                                                                                                                                                                                                                                                     Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPH-like receptor
                                                                                                    (BY SIMILARITY)
                          998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC
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 Gaps
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DEPAT_MOUSE STANDARD; PRT; 998 AA.

Q61772; Q61773; Q61774; Q61505;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

Q1-NOV-1997 (Rel. 35, Last annotation update)

D1-NOV-1997 (Rel. 35, Last annotation update)

EPHARIN TYPET-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3) (EMBRYONIC BRAIN KINASE) (EBK) (DEVELOPMENTAL KINASE 1) (MDK-1).

EPHA7 OR EHK3 OR EBK OR MDK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ellis J., Liu Q., Breitman M., Jenkins N.A., Gilbert D.J., Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling Fletcher F.A., Ziegler S.F., Rogers J.H.;
"Embryo brain kinase: a novel gene of the eph/elk receptor kinase family.";
Mech. Dev. 52:319-341(1995).
Mech. Dev. 5
                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 96081374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDK1, a novel receptor nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
STRAIN-BALB/C; TISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148
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Identification of alternatively spl
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                                                                                                                                            MDK1.

TISSUE SPECIFICITY: WIDELY EXPRESSED IN EMBRYO. IN ADULT, TISSUE SPECIFICITY: WIDELY EXPRESSED IN EMBRYO. IN ADULT, EXPRESSION RESTRICTED TO HIPPOCAMPUS, TESTIS AND SPLEEN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATT DOMAIN. BELONGS TO THE EPHRAIN RECEPTOR FAMILY.
DOMAIN. BELONGS TO THE EPHRAIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
ween the Swiss Institute of Bloinf.
European Bioinformatics Institute.
by non-profit institute.
                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (MDK1, MALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN (MDK1, MDK1-2) ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                   SPLICING
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JR PRINTS; PR00014; TYRKINASE.

DR PRINTS; PR00109; TYRKINASE.

DR PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.

DR PROSITE; PS00019; RECEPTOR_TYR_KIN_V_1; 1.

DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

DR PROSITE; PS001186; EGF_2; UNKNOWN_1.

DR PROSITE; PS001186; EGF_2; UNKNOWN_1.

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IN ISOFORM MDK1-1).

MISSING (IN ISOFORM MDK1-2).

MISSING (IN ISOFORM MDK1-1).

MISSING (IN ISOFORM MDK1-T1).

FKFPGTKTYID -> SLVTNEHLSYL (IN ISOFORM MTK1-T1).

FKFPGTKTYIDPETYEDPNRAVHOPAK -> SLYRERGDGM EXTOHNKKWMIASCSRL (IN ISOFORM MDK1-T2).

MISSING (IN ISOFORM MDK1-T2).
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FIBRONECTIN TYPE-III.
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ALIGNMENTS

A; Molecular type: protein
A; Molecular type: protein
A; Residues: 21-39,810-860 <WIZ>
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea C; Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas F; 11-20/Domain: signal sequence *status predicted <SIG>
F; 21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
F; 619-885/Domain: transmembrane *status predicted <TMM>
F; 619-885/Domain: protein kinase homology <KIN>
F; 627-635/Region: protein kinase ATP-binding motif
F; 232,337,391,404,493/Binding site: carbohydrate (Asn) (covalent) *status predicted protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) Thec-1993 #text_change 18-Jun-1999 C;Accession: A38224 B38224 C;Accession: A38224, B38224 B38224;MUID:92179233 A;Fitle: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expre A;Reference number: A38224; MUID:92179233 A;Accession: A38224; MUID:92179233 B;Accession: A38224 B3824 B;Accession: A38224 B3824 B3 Q 밁 В 뮍 밁 ğ δÃ Š 밁 Š A;Molecule type: mRNA
A;Residues: 1-983 <WIC>
A;Cross-references: GB.M83941; NID:g183931; PIDN:AAA58633.1;
A;Experimental source: pre-B-cell leukemia cell line LK63
A;Note: sequence extracted from NCBI backbone (NCBIP:86627)
A;Accession: B38224 Query Match
Best Local Similarity
Matches 271; Conserv 241 181 181 121 121 61 61 RMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 271 LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP NLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFY 180 HYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETF HYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETF 120 RMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP 100.0%; ilarity 100.0%; Conservative 0 0 Score 1466; DB 2; Pred. No. 2.9e-122; Mismatches 271 0, Indels Length PID:g183932 0, Gaps 180 120 60 60 240 240 0,

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A, Status: preliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-983 <SAJ>
A, Cross-references: GB.M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A, Cross-references: GB.M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A, Note: sequence extracted from NCBI backbone (NCBIN:62398, NCBIP:62401)
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type
C; Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F;619-885/Domain: protein kinase homology <KIN>
F;627-635/Region: protein kinase ATP-binding motif
                                                                             A;Cross-references: GB:M68514; NID:g454809; PIDN:AAA48666.1; PID:g211447 A;Note: sequence extracted from NCBI backbone (NCBIN:62405, NCBIP:62411) C;Superfamily: protein-tyre kidase, receptor tyre eph; fibronectin tyre C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein F;619-885/Domain: protein kinase homology <KIN> F;627-635/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                          receptor tyrosine kinase Cek4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: B45583
R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A;Title: Identification of a new eph-related receptor tyrosine kinase gene;
A;Reference number: A45583; MUID:92031278
A;Recession: B45583
A;Status: preliminary
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C;Date: 22-Apr-1993 #sequence_revision
C;Accession: A45583
R;Sajjadi, F.G.; Pasquale, E.B.; Subram
New Blol. 3, 769-778, 1991
A;Title: Identification of a new eph-re
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A; Residues: 1-983 <SAJ>
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    Similarity 91.
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95.9%;
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91.6%;
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   Score 1309; D
Pred. No. 2.6e
8; Mismatches
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Pred. No. 1.9e-116;
Pred. No. 1.9e-116;
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C;Superfamily: protein tyrosine kinase, receptor C;Keywords: ATP; transmembrane protein F;628-936/Domain: protein kinase homology <KIN>F;636-644/Region: protein kinase ATP-binding moti
 receptor protein-tyrosine kinase - C:Species: Homo sapiens (man) C:Date: 29-May-1998 #sequence_revi:
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178844
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A;Molecule type: mRNA
A;Residues: 1-948 <MAI>
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C;Accession: S51605
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C; Species: Rattus norvegicus (Norway rat)
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 #sequence_revision
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                                  human
 29-мау-1998
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#text_change
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R;Malsonplerre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D. Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph re A;Reference number: S49015; MUID:94067777
                                                                         EEISGYDEHYTPIRTYQYCNYMDHSQNNWLRTNWYPRNSAQKIYYELKETLRDCNSIPLY
                                                                                                                                                                                                                         CEVREFUL-----QFGFFLPLLTAWTGDCSHVSNQVVLLDTSTVMGELGWKTYPLNGW
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PIERKGFYLAFQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCV
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Pred. No. 4.1e-81;
9; Mismatches 37;
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18-Jun-1999

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RESULT 6
148967
brain-specific kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148967
R;Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz, N.T.
J. Neurosci. Res. 37, 129-143, 1994
A;Title: Isolation and characterization of Bsk, a growth factor receptor-lil
A;Reference number: 148967; MUID:94194581
A;Reference number: 148967; MUID:94194581
A;Accession: 148967
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C:Superfamily
F:619-885/Dom
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R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, Oncogene 10, 897-905, 1995
A;Title: cDNA cloning and tissue distribution of five human EPH-like receptory. A;Reference number: 158351; MUID:95206782
A;Accession: 178844
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-986 <RES>
A;Cross-references: GB:L36645; NID:g551613; PIDN:AAA74246.1; PID:g551614
C;Genetics:
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C;Superfamily: protein-tyrosine kinase, receptor
C;Superfamily: protein-tyrosine kinase, receptor
C;Keywords: ATP; transmembrane protein
F;512-778/Domain: protein kinase homology <KIN>
F;520-528/Region: protein kinase ATP-binding moti
F;801-868/Domain: SAM homology <SAM>
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A;Residues: 1-877 <RES>
A;Cross-references: EMBL:U07357; NID:g466369; PIDN:AAA17038.1; PID:g466370
C;Genetics:
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Best Local Similarity
Matches 183; Conser
                                                                                                Query Match
Best Local Similarity
Matches 174; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat:619-885/Domain: protein kinase homology <KIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYME
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                                           LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPGVMGTCKETFNLYYYE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADGEWLYPIGNCLCNAGHEERSGECQ 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSCVNNSEEKDVPKMYCG
                             LLLCAALRT - - - LLASPSNEVNLLDSRTVMGDLGWIAFPKNGWEEIGEVDENYAPIHTYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDNDKERFIRENQFVKIDTIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFQDV
                                                                                                                                                                                    protein kinase homology <KIN>
protein kinase ATP-binding mo
SAM homology <SAM>
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                                                                                                                   67.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                Score 990; DE
Pred. No. 5.3e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 995; DB 2;
Pred. No. 2.2e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Bsk, a growth factor receptor-like tyrosine
                                                                                                                                                                                                       motif
                                                                                                DB 2; 1
3e-80;
les 41;
                                                                                                                                                                                                                                                        type
                                                                                                                               Length 877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 986;
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C;Superfamily: protein-tyrosine kinase, receptor type C;Keywords: ATP; transmembrane protein F;568-834/Region: protein kinase homology <KIN>F;576-584/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-898 <TAY>
A;Cross-references: EMBL:X78689; NID:g531543; PIDN:CAA55357.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Taylor, V.; Pfarr, S.; Miescher, G.C.; Honegger, submitted to the EMBL Data Library, April 1994
A;Description: Expression and developmental regula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor tyrosine kinase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Accession: S47489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
S47489
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                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.4
Best Local Similarity 66.2
Matches 174; Conservative
                                                                                                             190
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                                                                                                                                          DHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGAC 189
                                                                                                                                                                                                                     VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD 167
                                                                                                                                                                                                                                                                                          LLLCAALRT---LLASPSNEVNLLDSRTVLGDLGWIAFPKNGWEEIGEVDENYAPIHTYQ 107
                                                                                                                                                                                                                                                                                                                LLSCSYLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ 69
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                                                                                                                                                                                                                                                          VCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD 129
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EWLVPIGKCMCKAGYEEKNGTCQ
                                EWLVPIGKCSCNAGYEERGFMCQ 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S47489
                                                                                                                                                                                                                                                                                                                                                                    67.4%; Score 988; DB 2; 66.2%; Pred. No. 8.2e-80; Live 44; Mismatches 41
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receptor-like

tyrosine

kinase

28-May-1999

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receptor-like tyrosine kinase Ehk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C:Accession: S51604
R:Malsonplerre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosi
A;Reference number: S49015; MUID:94067777
A;Accession: S51604
A;Status: preliminary
A;Crossion: F51604
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-981 <MAID
A;Cross-references: EMBL:S68029
A;Cross-references: EMBL:S68029
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Reywords: AFP; transmembrane protein
C;Reywords: AFP; transmembrane protein
C;Reywords: AFP; transmembrane protein
F;651-917/Domain: protein kinase homology <KIN>
F;659-667/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S51603
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-893 <MAIN
A;Cross-references: EMBL:S68028
A;Cross-references: EMBL:S68028
A;Cross-references: EMBL:S68028
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin
C;Keywords: ATP; transmembrane protein
C;Keywords: ATP; transmembrane protein
F;563-829/Domain: protein kinase ATP-binding motif
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Best Local S
Matches 173
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Best Local S
Matches 173
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                                                                                                                          LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ 69
                                                                         VCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGAC 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLCAALRT --- LLASPSNEVNLLDSRTVLGDLGWIAFPKNGWEEIGEVDENYAPIHTYQ 102
                    DHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGAC
                                                        VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173;
                                                                                                                                                                                                     Similarity 65.8
73; Conservative
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67.2%;
65.8%;
                                                                                                                                                                                                                     67.28;
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                                                                                                                                                                                                      <u>4</u>5;
                                                                                                                                                                                                   Score 985; DB 2;
Pred. No. 1.7e-79;
5; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.5
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No. 1.
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.5e-79;
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A;Status: proliminary
A;Molecule type: mRNA
A;Residues: 1-305,'G',359-1005 <MA2>
A;Cross references: EMBL:S68026
A;Note: the authors translated the codon GAC for re
C;Superfamily: protein tyrosine kinase, receptor ty
C;Keywords: ATP; transmembrane protein
E;675-941/Domain: protein kinase homology <KIN>
F;683-691/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-U1-1995 #sequence_revision 21-Ju1-1995 #text_change
C;Accession: S49015; S51602
R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-
A;Reference number: S49015; MUID:94087777
A;Accession: S49015
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S49015
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A; Residues: 1-1005 <AAI>
A; Cross-references: EMBL:S68024
A; Note: the authors translated
A; Accession: S51602
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                                                                               VALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG
EWLVPIGKCMCKAGYEEKNGTCQ
                                                                                                                              ENGRNIKONQYIKIDTIAADESETELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVGAC
                                                                                                                                                  DHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGFVNKKGFYLAFQDVGAC
                                                                                                                                                                                              VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLFGGLGTCKETFNMYYFESDD
                                                                                                                                                                                                                  VCNYMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD 129
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                                EWLVPIGKCSCNAGYEERGFMCQ
                                                                 IALVSVRVYYKKCPSVVRHLAVFPDTITGADSSQLLEVSGSCVNHSVTDDPPKMHCSAEG
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                                                                                                                                                                                                                                                                                                                                                 Similarity
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65.88;
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Pred. No. 1.7e-79;
5; Mismatches 41
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receptor protein-tyrosine kinase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C;Accession: I78843
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, Oncogene 10, 897-905, 1995
A;Title: cDNA cloning and tissue distribution of five human EPH-like receptors

Basu,

protein

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A;Accession: SJULLE
A;Accession: SJULLE
A;Accession: SJULLE
A;Molecule type: mRNA
A;Residues: 1-31,55-986 <GILLE
A;Residues: 1-31,55-986 /GILLE
C;Reperfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III r
C;Reperfamily: protein-tyrosine kinase predicted <SIG>
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-986/Product: protein-tyrosine kinase Eph #status predicted <MAT>
F;548-569/Domain: protein kinase homology <KIND
F;627-635/Region: protein kinase homology <KIND
F:027-635/Region: protein kinase ATP-binding motif
F:098-974/Domain: SAM homology <SAMD
T:098-974/Domain: sam homology <SAMD
T:098-974/Domain: sam homology <SAMD
T:098-974/Domain: protein kinase ATP-binding motif
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S78059
                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X65138; NID:g54083; PIDN:CAA46268.1; PID:g54084 R;G1lard1-Hebenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chestier, Oncogene 7, 2499-2506, 1992 A;Title: An Eph-related receptor protein tyrosine kinase gene segmentally (A;Reference number: S30496; MUID:93096484 A;Accession: S30505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - C;Species: Mus musculus (house mouse) C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #te: C;Accession: S78059; S30505; I58366 R;Charnay, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, A; Reference number: $78059
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F; 627-893/Domain:
F; 916-982/Domain:
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A; Residues: 1-986 <CHA>
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A; Residues: 1-991 <RES>
A; Cross-references: GB:L36644;
C; Genetics:
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A; Accession: 178843
A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession:
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Best Local S
Matches 173
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in: protein kinase homology
in: SAM homology <SAM>
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65.8%;
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Pred. No. 2.1e-79;
4; Mismatches 42
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A;Gene: Pag
C;Superfamily: protein-tyrosine kinase, receptor type (C;Superfamily: protein-tyrosine kinase, receptor type (C;Keywords: ATP; transmembrane protein
F;618-884/Domain: protein kinase homology <KIN>
F;628-634/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Winning, R.S.; Sargent, T.D.
Mech. Dev. 46, 219-229, 1994
A;Title: Pagliaccio, a member of the Eph
A;Reference number: I51549; MUID:95001564
A;Accession: I51549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Xenopus laevis (African claw C; Date: 13-Sep-1996 #sequence_revision
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A; Residues: 1-985 <WIN>
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                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                                         Query Match
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 267
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||||||||::||||::||||::||||
TIAADESETQVDIGDRIMKLNTEVRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL 206
                                                                 .TVRNLAQFPDTITGSDTSSLVEVRGSCVDNSEEKDVPKMYCGADGEWLVPIGNCLCNAGF
                                                                                                                                                                                                                     NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIAADESETQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF 204
EEHNGGCQ
                               EERGFMCQ
                                                                               TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGY 263
                                                                                                                                                                                                                                                                                      PSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT 84
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                                                                                                                                                                                                 DWIPRSGAQRVYVEIKFTLRDCNSLPGVMGTCKETFNLYYYESNNDKERFIRETQYVKID 146
                                                                                                                                                                                                                                                                    PASEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMESSQNNWLRT 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWITREGAORVYIEIKFTLRDCNSLPGVMGTCKETFNLYYYESDNDKERFIRESOFGKTD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PANEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMEASQNNWLRT 86
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70.6%;
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35; Mismatches
                                                                                                                                                                                                                                                                                                                                       Score 977; DB 2;
Pred. No. 8.7e-79;
9; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from GB/EMBL/DDBJ
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ches 34;
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RESULT

repea

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A;Reference number: 158
A;Accession: 158351
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-998 <RESy
A;Cross-references: GB:
                                                                A; RCCESSION: 1000-7

A; Klatus: translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residues: 1-279, 444-572, 'R', 596-1013 <SI3>
A; Cross-references: EMBL:U03910; NID:g555617; PIDN:AAB60614.1
C; Genetics:
A; Gene: Cek7
C; Superfamily: protein-tyrosine kinase, receptor type eph; f1
C; Keywords: alternative splicing; ATP; transmembrane protein
F; 649-915/Domain: protein kinase homology <KIN>
F; 657-665/Region: protein kinase ATP-binding motif
F; 938-1004/Domain: SAM homology <SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor-type protein-tyrosine kinase Cek7, long splice form - chicken C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C;Accession: I50615; I50616; I50614
R;Slever, D.A.; Verderame, M.F.
Gene 148, 219-226, 1994
A;Title: Identification of a complete Cek7 receptor protein tyrosine kinase A;Reference number: I50614; MUID:95047429
                                                                                                                                                                             receptor protein-tyrosine kinase - human
C;Species: Homo sapiens (man)
C;Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Accession: I50614
A;Accession: I50614
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A;Accession: I50615
A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-1013 <SIE>
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Matches 170
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                                                       preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCNYMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD 129
                                                                                                                                                                                                                                                                                                                  EWLVPIGKCLCKAGYEEKNNTCQ
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                                                                                                                                                                                                                                                                                                                                                                                       IALVSVRVYYKKCPSVIRNLARFPDTITGADSSQLLEVSGVCVNHSVTDEAPKMHCSAEG
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                      <RES>
                                                                                                                                           P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu,
 GB:L36642; NID:g551607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.68;
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Pred.
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No. 4.2e-76;
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 PIDN:AAA74243.1;
                                                                                                        of five human EPH-like receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1013;
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PID: g551608
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C;Genetics:
A;Gene: HEKII
C;Superfamily: protein-tyrosine kinase, receptor ty
C;Keywords: ATP; transmembrane protein
F;631-897/Domain: protein kinase homology <KIN>
F;639-647/Region: protein kinase ATP-binding motif
F;920-986/Domain: SAM homology <SAM>
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                                                                                               QPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT 84
                                               TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKE--EDPPRMYCSTEGEWLVPIGKCSCNA 261
                      GYEERGFMCQ 271
                                                                                                                                                              NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID 144
                                                                                                                                                                                                   QAAKEVLLLDSKAQQTELEWISSPPNGWEEISGLDENYTPIRTYQVCQVMEPNQNNWLRT 87
                                                                                                                                                 NWISKGNAORIFVELKFTLRDCNSLPGVLGTCKETFNLYYYETDYDTGRNIRENLYVKID
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                              63.3%; Score 927.5; DB 2 68.4%; Pred. No. 2.2e-74;
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Search completed: May 9, 2000, 22:27:20 Job time: 4159 sec

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Post-processing: Minimum Match 0%
Listing first 45
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Maximum DB
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Perfect score:
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length: 1000000
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Gapop 10.0 , Gapext 1.0
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   Result
                                                         Pred. No. is the score greater that and is derived
                                                      No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
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em_est25:
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gb_est30:*
gb_est31:*
gb_est31:*
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em_gss11:
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gb_gss11:
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                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
                                                                                                                                                                                H38363 435 bp mRNA EST 16-AUG-1995 yp50g04.rl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190902 5' similar to gb:M83941 TYROSINE-PROTEIN KINASE RECEPTOR HEK PRECURSOR (HUMAN); mRNA sequence. H38363 GI:907862
The WashU-Merck EST Project Unpublished (1995)
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AU315344

AI3249967

AI3249967

AI3249967

AI333334

AI3323334

AI33233340

AI346937

AI8789781

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AIO11632 ESTZÓ6082
AIO11632 ESTZÓ6083
B36983 HS-1042-A2
AI325344 mIO1CO2.y
AI325344 mIO1CO2.x
AI325967 gravardo2.x
AAO24123 mIO1CO2.x
AI323334 mIO1CO2.x
AI333334 mIO1CO2.x
AI333334 mIO1CO2.x
AI337308 t550801.x
AII06200 vIII1604 x
AW045268 UI-W-BH1.
AII079781 DKEZP434M
H25851 y153903.s1
AW233440 fj22f03.s1
AW333440 fj22f03.s1
AW33440 fj22f03.s1
AW3445840 fj22f03.s1
AW3446840 fj22f03.s1
AW3446840 fj22f03.s1
AW344684
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AA746914 nx69402.s

AW017395 EST272817

AW256663 EST304800

A1366919 qv94h06.x

AI143874 qe04f05.x

AI112217 UI-R-Y0-m

AL098595 Drosophil
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          363
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On May 5, 1995 this sequence version replaced gi:797807.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 2663
High quality sequence stops: 276
Source: IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2663
Std Error: 0.00
Seq primer: M13Rev
                                                                                                                                                                                                                                                   CACTCTACGAGACTGCAATAGCATTCCATTNGTTTTAGGNACTTNCAAGGGGACATTAAC
                cactctacgagactgcaatagcattccattggttttaggaacttgcaaggagacattcaa
                                                            GCTGAGAACAAACTGGGTCCCCAGGAACTCAGCTCAGAAGATTTATGTGGAGCTCAAGTT
                                                                             gctgagaacaaactgggtccccaggaactcagctcagaagatttatgtggagctcaagtt
                                                                                                                         TTACACACCCATCAGGACTTACCAGGTGTGCAATGTCATGGACCACAGTCATAACAATTG
                                                                                                                                          ttacacacccatcaggacttaccaggtgtgcaatgtcatggaccacagtcaaaacaattg
                                                                                                                                                                                          GCTGGGCTGGATCTCTTATCCATCACATGGGTGGGAAGAGATCAGTGGTGTGGATGAACA
                                                                                                                                                                                                            gctgggctggatctcttatccatcacatgggtgggaagagatcagtggtgtgggatgaaca
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52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: p7773D (Pharm
modified polylinker; Site_1: Not I; Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:3847311"
/db_xref="taxon:9606"
/clone="IMAGE:190902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares retina
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                               42.98;
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5.4e-96;
hes 9;
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            atcaggacttaccaggtgtgcaatgtcatggaccacagtcaaaaccaattggctgagaaca 252
                                                                                              CCCGCGAATGAAGTTACTTTATTGGATTCCAGATCTGTTCAGGGAGAGCTTGGGTGGATA 194
                                                                                                                                             TTCATCCTCTTTTCGTTTCTCTTTGGAATTTGCGACGCTGTCACCGGTTCTAGGGTATAC 134
                                                                                                                                                                      tccatcctcctcctcagctgctctgttctcgacagcttcggggaactgattccgcag 75
                                                             tcttatccat---cacatgggtgggaagagatcagtggtgggatgaacattacacaccc 192
                                                                                                              GCAAGCCCTCTGGAAGGAGGG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 835)
Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R.,
Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mou
library made by oligo-capping method
Unpublished (1999)
On May 18, 1998 this sequence version replaced
Contact: Katsuyuki Hashimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institute of Infectious Diseases 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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AU080921.1
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AU080921 Sugano mo
5', mRNA sequence.
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                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                       Sugano mouse brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="MNCb-6241"
/clone_lib="Sugano mouse
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Metazoa;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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Sciurognathi; Muridae;
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                                                                                                                                Unpublished (1999)
On Jun 5, 1998 this sequence version re
Other_ESTS: fi31g02.x1
Contact: S.L. Johnson
Washington University School of Medicir
4444 Forest Park Parkway, Box 8501, St
Tel: 314 286 1810
Fax: 314 286 1810
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1 (bases 1 to 572)
1 (bases 1 to 572)
Sugano, S., Kawakami, K., Johnson, S., Li, F., Maxra, M., Eddy, S., Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T., Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B., Ritter, E., Bowers, F., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW175051 572 bp mRNA EST fi31902.y1 Sugano Kawakami zebrafish DRA Danio 2639282 5 similar to SW.EPA4_CHICK Q07496 EPHR
                                              Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Sugano
Sequencing by: Washington University Gen
Seq primer: T3 ET from Amersham
High quality sequence stop: 485.
                                                                                                                                                                                                                                                                        WashU
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/organism="Danio rerio
                               Location/Qualifiers
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Matches 306; Conserv
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EST206082 Normalized r
ROVAX55 3' end, mRNA s
AI011631
AI011631.1 GI:3225463
Rattus sp.
Rattus sp.
Eukaryota;
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/db_xref="taxon:7955"
/clone="2639282"
/clone_lib="Sugano Kawakami zebrafish
/sex="mixed (one male and one female,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unfertilized eggs)"
/dev_stage="adult"
     Metazoa;
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Chordata; Craniata; Vertebrata;
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d rat ovary,
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Pred. No. 8e-51;
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Best Local S
Matches 268
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Local Similarity 57.1%;
hes 268; Conservative
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                                                                                                                                     tcaacactgagattagagaagtaggtcctgtcaacaagaagggatttta 539
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                                                                                                                                                                                            ACACCATCGCCCCTGACGAGATCACGGTCAGCAGTGACTTCGAGGCTCGCAATGTCAAGC
                                                                                                                                                                                                                                                                                                                    GAGACTGCAATAGCTTTCCGGGTGGCGCCAGCTCCTGCAAAGAGACCTTCAACCTCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seg primer: M13-21.
AI011632 473 bp mRNA
EST7206083 Normalized rat ovary
ROVAX56 3' end, mRNA sequence
AI011632
AI011632.1 GI:3225464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
On Jan 19, 1998 this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene
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1 (Dases 1 to 474)
Lee.N.H., Glodek, A., Chandra, I., Mason, T.M.,
Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Genome Project: Generation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus sp."
/db_xref="ArCC (inhost):2021827"
/db_xref="ArCC (inhost):2021827"
/db_xref="taxon:01118"
/clone="ROVAX55"
/clone="ROVAX55"
/clone="Toyan: ovary; Vector: pT7T3Pac; Site_2: NotI"
7 a 129 c 135 g 93 t
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Pred. No. 2.8e-34;
0; Mismatches 201;
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                                             Rattus
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Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 473)
Lee.N.H., Glodek,A., Chandra,I., Mason,T.M., Quacken
Kerlavage,A.R. and Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute for Genomic Research 9712, Medical Center Drive, Rockville, Tel: (301)-838-5529
Fax: (301)-838-0208
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On Jan 19, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: nhlee@tigr.org
Seg primer: M13-21.
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/clone_lib="Normalized rat ovary, Bento Soares"
/note="0rgan: ovary; Vector: pT7T3Pac; Site_1:
Site_2: Not!"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus sp."
/db_xref="ATCC (inhost):2021828"
/db_xref="taxon:10118"
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                                                                                                                                                                aagatcctccaaggatgtactgcagtacagaaggcgaatggcttgtacccattggcaagt 769
                                                                                                                                                                                                                                actcccagtccctggtggaggttagagggtcttgtgtgtcaacaattctaagga-----gg 709
                                                                                                                                                                                                                                                                                                    aaaagtgcccatttacagtgaagaatctggctatgtttccagacacggtacc---catgg 655
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                                                                                GTATCTGCA/AGCAGGCTACCAGCAAAAAGGAGACACTTGTGAA
                                                                                                                                                AAAACGCCCCCAGGATGCACTGCAGTGCAGAAGGAGAATGGTTAGTGCCCATTGGAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Construction of a Characterized Clone Resource for
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Class: BAC ends
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1 (bases 1 to 424)
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E-Coli DH10B"
77 c 101 g 122 t 1 others
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/db_xref-"taxon:9606"
/clone-"plate=CT 824 Col=10 Row-K"
/clone_lib-"CIT Human Genomic Speri
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DEFINITION

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                                                                                          CCCTATGGCAAAGGGTGGGACCTGATGCAGAACATCATGGACGACATGCCTATCTACATG
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. LK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 406)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone IMAGE:459170 5' similar to gb:U07634 Mus musculus receptor-protein tyrosine kinase (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800 Fax: 314 286 1810
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Location/Qualifiers
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                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                   79
                                                                                                                                                                                                                                                                                                                                           T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

a 117 c 109 g 100 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares mouse
/sex="unknown"
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                                                                                                                                                                                                                                                        Score 126.8;
Pred. No. 5.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Fax: 314 286 1810

Email: est@vatson.wustl.edu

Insert Size: 1695

High quality sequence stops: 337 Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1695

Std Error: 0.00
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1 (bases 1 to 402)

1 (this to
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On Sep 21, 1992 this sequence
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                    108
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:401890"
/db_xref="taxon:9606"
/clone="IMAGE:29543"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares infant brain
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                                                               1 Similarity
218; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 493)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI249967 493 bp mRNA qx47d02.x1 NCI_CGAP_Pan1 Homo sapiens similar to gb: M59371 TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                unknown library type
Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

a 141 c 142 g 101 t 2 others
                                                                                                                                                                                                                                                       /clone="TMAGE:2004483"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                          Score 112.2; DB 44;
Pred. No. 1.6e-23;
0; Mismatches 159;
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Pred. No. 1.1
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1.1e-25;
hes 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 314 60 2020
Email: mouseesfewatson.wustl.edu
This clone is available royalty free through LLNL;
This clone is available royalty free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA024123 366 bp mRNA EST 21-JAN-1997 millcO2.rl Soares mouse placenta 4NbMpl3.5 14.5 Mus musculus clone IMAGE:459170 5' similar to gb:U07634 Mus musculus receptor-protein tyrosine kinase (MOUSE);, mRNA sequence. AA024123 AA024123.1 GI:1489009
                                                                                                                                                                                                                                                                                                                                                  WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                       On May 8, 1995 this sequence version Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 366)
                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                    IMAGE Consortium (info@image.llnl.gov)
MGI:276058
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                 primer: -28M13 rev2 from Amersham
                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459170"
/note="Organ: placenta; Vector: pT7T3D-Pac
with a modified polylinker; Site_1: Not I;
                                                      /tissue_type="placenta"
/dev_stage="adult"
                                                                                         /sex="unknown"
                                                                                                       /clone_lib="Soares mouse
                                                                                                                                                                                                             Location/Qualifiers
                                      'lab_host="DH10B"
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Louis,

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contact the

gi:800409

Mus

Mammalia;

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(Pharmacia) Site_2: Eco

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169;
                                                                                                                                                    On Jan 17, 1998 this sequence version repl
Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI323334 348 bp mRNA EST 23-DEC-1998 millicol.x1 Soares mouse placenta 4NbwP13.5 14.5 Mus musculus cDNA clone IMAGE:459170 3' similar to gb:M59371 TYROSINE-PROTEIN KINASE RECEPTOR ECK PRECURSOR (HUMAN); gb:U07634 Mus musculus receptor-protein tyrosine kinase (MOUSE); mRNA sequence.
AI323334
                                                                                                                                                                                                                                                                                                                                                          Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 348)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa;
                     This clone was previously sequenced on data is from the 3' end
                                                                                                                                                                                                                                                                                                                    Unpublished (1996
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considered
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103 c 102 g 92 t
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overall
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poor
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                                                                                                                                                                                    A1337308 496 bp mRNA EST 18-MAR-1999 tb98b01.x1 NCI_CGAP_CO16 Homo sapiens cDNA clone IMAGE:2062345 3' similar to SW:EPB2_HUMAN P29323 EPHRIN TYPE-B RECEPTOR 2 PRECURSOR CONTAINS element MER22 repetitive element ; mRNA sequence.

A1337308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertu
Eutheria; Primates; Catarrhini; Hominidae; H
I (bases 1 to 496)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                    EST
                Tumor
                                                                                                                                        human
                                                                                                                                                                        AI337308.1
                              National Cancer Institute,
                                                                                                                    Homo sapiens
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            Gene Index
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94 c 93 g 74 t
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with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:459170"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="placenta"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism≃"Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib~"Soares mouse
                                                                                                                                                                        GI:4074235
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                                                                                  Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 103.2; DB Pred. No. 8e-21; 0; Mismatches 14
                              Cancer Genome Anatomy Project (CGAP),
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RESULT 13
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           DEFINITION
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Best Local Similarity
Matches 204; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     aaggagacattcaacctgtactacatggagtctgatgatcatg-----gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9t9gagctcaagttcactctacgagactgcaatagcattccattggttttaggaacttgc 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCCAGAACAACTGGCTACGGACCAAGTTTATCCGGCGCGCGTGGCGCCCACCGCATCCAC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agtcaaaaccaattggctgagaacaaactgggtccccaggaactcagctcagaagatttat 288
                                                                                                                     GTGCC
                                                                                                                                                                                     CCTGTGTCCCGCAGCGGCTTCTACCTGGCCTTCTACTGTAACGGGGACGGCGAGTGGCTG
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                                                                                                                                                                                                                                                                 TCCCAGGTGGACCTGGGTGGCCGCGTCATGAAAATCAACACCGAGGTGCGGAGCTTCGGA
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                                                                                                                                                    gtgtc
                                                                                                                                                                                                                                                                                                                                        CCCAACTGGATGGAGAATCCATGGGTGAAGGTGGATACCATTGCAGCCGACGAGAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                AAGGAGACCTTCAACCTCTATTACTATGAGGCTGACTTTGACTCGGCCACCAAGACCTTC 190
 AW045268 314 bp mRNA EST UI-M-BH1-akn-b-03-0-UI.S1 NIH_BMAP_M_S2 Mus
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                     375
                                                                                                                                                        581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Colo was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).

Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2062345"
/clone_lib="NCI_CGAP_Co16"
/tissue_type="colon tumor,
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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55.9%;
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     musculus cDNA clone
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                       18-SEP-1999
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AUTHORS
TITLE
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MEDLINE
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   141
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TACTCGGTGTGCAACGTGGTATCCGGCGACCAGGACAACTGGCTCCGCACCAACTGGGTG
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Query Match
Best Local S
Matches 164
                                                                                                                                                                                                                                                                                                82 aatgaagtcaatctactggattcaaaaacaattcaaggggagctgggctggatctcttat 141
taccaggtgtgcaatgtcatggaccacagtcaaaacaattggctgagaacaaactgggtc 261
                                                                                                CCCTATGGCAAAGGGTGGGACCTGATGCAGAACATCATGGACGACATGCCTATCTACATG 140
                                                                                                                                                                        ccatcacatgggtgggaagagatcagtggtgtggatgaacattacacacccatcaggact 201
                                                                                                                                                                                                                                                    164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I si
is likely internal to the message.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 Forward POLYA=No.
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Fax: 301 443 9890
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20892-9643, USA
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National Institute of Mental Health
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Rodentia;
1 (bases 1 to 314)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted libraries from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted libraries from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted libraries from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted libraries from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted libraries from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted libraries from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted library derived from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted library derived from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted library derived from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted library derived from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted library derived from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted library derived from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted library derived from ten regions of the mouse brain (cerebellum, brain stems, lefetor: balls to be a subtracted library derived from ten regions of the mouse brain (cerebellum, brain stems).
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84 c
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TAG_LIB-NIH_BMAP_M_S2
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/clone_1ib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 89; DB 64;
Pred. No. 1.7e-16;
0; Mismatches 126
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                                                                                                                                                                                                                                                                                       Local Similarity
acagtgaagaatctggctatgtttccagacacggtacccatggactcccagtcc---ctg
                                                                                                                                       agcattccattggttttaggaacttgcaaggagacattcaacctgtacta 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cccaggaactcagctcagaagatttatgtggagctcaagttcactctacgagactgcaat
                                                                                      GACATAGGTGCCTGGCCATCCTCTCTCTCCGCATCTATAAGAAGTGCCCTGCC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTTCCCGGGTGGCGCCAGCTCATGCANAGAGACCTTCAACCTCTACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189146.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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DNA Sequencing by: Washington University Jenome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI_CGAP_GC4 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared and a prepared and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:2516671"
/clone_lib="NCI_CGAP_GC6"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                  10.8%;
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                                                                                                                                                                                                                                             Score 88.2; DB 63;
Pred. No. 3.3e-16;
0; Mismatches 88;
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Best Local Similarity 60.3
Matches 143; Conservative
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                                                                   ATGACATGCCGATCTACATGTACTCCGTGTGCAACGTGATGTCTGGCGACCAGGACAACT 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=ILO&t2=ILO-HT0156-
251099-132-a12&t3=1999-10-25&t4=1)
Seq_primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
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On Mar 16, 1998 this sequence version replaced g1:2961824.
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1 (bases 1 to 344)
HCGP http://www.ludwig.org.br/ORESTES.
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/note="Organ: h
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Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches
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Listing first 45 summaries
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1: /cgn2_6/ptodata/2

2: /cgn2_6/ptodata/3

3: /cgn2_6/ptodata/3

4: /cgn2_6/ptodata/5

5: /cgn2_6/ptodata/7

7: /cgn2_6/ptodata/7
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-715-106-9
US-08-162-809-15
US-08-469-537A-102
US-08-449-248-1
US-08-449-645A-14
US-08-449-645A-14
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US-08-49-645A-16
US-08-702-367A-16
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US-08-702-367A-16
US-08-702-367A-16
US-08-702-367A-12
US-08-162-809-21
US-08-162-809-21
US-08-162-809-19
US-08-162-809-17
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Sequence 15, Appli
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Sequence 14, Appli
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US-08-167-919A-9
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Patent No.
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23,	ر ر	Sequence 23, Appl	Sequence 5, Appli	Sequence 1, Appli	Sequence 4, Appli	ω	Sequence 4, Appli		Sequence 2, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 13, Appl	9, A	Sequence 10, Appl	•	Sequence 10, Appl	Sequence 11, Appl

ALIGNMENTS

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APPLICATION UMBER: US/08/167,919A
FILING DATE: 18-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-UN-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/AU92/00294
FILING DATE: 19-UN-1992
ATTORNEY/ACHT INFORMATION:
NAME: D1619110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPAN: (516) 742-4343
TELEFAX: (516) 742-4343
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                                           TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
  SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pair
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MEDIUM TYPE: Floppy disk
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CITY: Garden City
STATE: New York
COUNTRY: Franchiscopies STATE: New York
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Ward, Larry D.
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TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
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RESULT 2 US-08-715-106-9 ; Sequence 9, Application

us/08715106

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; LOCATION:
US-08-715-106-9
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TELEPAS: (516) 742-4366
TELEZ: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6020306
GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richar
APPLICANT: Wicks, Ian
                                                                                                                                                                                                                                            Query Match

Best Local Similarity

Matches 813; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 911
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: D1G1g1lo, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: FEATURE:
                                                                                                                                                       121 gagctgggctggatctcttatccatcacatgggtgggaagagatcagtggtgtgggatgaa
                                                                                160
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STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                 gaactgattccgcagccttccaatgaagtcaatctactggattcaaaaaacaattcaaggg
GAGCTGGGCTGGATCTCTTATCCATCACATGGGTGGGAAGAGATCAGTGGTGTGGATGAA
                                                                           GAACTGATTCCGCAGCCTTCCAATGAAGTCAATCTACTGGATTCAAAAACAATTCAAGGG
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100..3048
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279
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RESULT 3
US-08-162-809-15
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            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                       APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NUVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS (
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
  ATTORNEY/AGENT INFORMATION:
                                                                                                                        ADDRESSEE: CAMPBELI
STREET: 4370 La Jo.
CITY: San Diego
STATE: California
COUNTRY: United St.
ZIP: 92122
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Best Local :
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                                            GAGGTGCGGGGTTCTTGTGTCAATCATTCCAAGGAGGAAGAGCCACCCAAGATGTACTGC
                                                        gaggttagagggtcttgtgtcaacaattctaaggaggaagatcctccaaggatgtactgc
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760 732 700 672 640 612 580 432

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STRANDEDNESS:
FEATURE:
NAME/KEY: CDS
LOCATION: 32
US-08-162-809-15
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                      641;
                           Similarity
                     Conservative
                                                                                     linear
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                    Score 545; DB 1; I
Pred. No. 1.4e-166;
0; Mismatches 160;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 476..349
US-08-469-537A-102
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US-08-469-537A-102
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                                                                                                                                                                    Query Match 43.2
Best Local Similarity 67.3
Matches 512; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: USON 469,537A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Rempler Ph.D., Gail M
REGISTRATION NUMBER: 32,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Maison
                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               Jy06 base pairs
Left: nucleic acid
STRANDEDNESS: nrt
TOPOLOGY
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MEDIUM TYPE: Disketi
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TITLE OF INVENTION: EHK AND
TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3906 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: REFERENCE/DOCKET NUMBER: REFERENCE: 114-345-7400
TELEPHONE: 914-345-7721
                    176
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CITY: Tarrytown
STATE: NY
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atgaacattaccacccatcaggacttaccaggtgtgcaatgtcatggaccacagtcaaa
                                             aaggggagctgggatctcttatccatcacatgggtgggaagagatcagtggtgtgg
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o. 5843749
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                                                                                                                                                                 Score 351.4; DB 3;
Pred. No. 6.7e-104;
0; Mismatches 246;
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APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/442,248 FILING DATE: 15-MAY-1995 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3:
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
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                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno CITY: South San Francisco
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Best Local Similarity
Matches 512; Conserv
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-8674
TELEFAX: 415/952-9881
     1415
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STRANDEDNESS: single
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TGTGCAAGGCCGGATATGAAGAGAAAAATGGTACCTGTCAA 1455
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                                                                   ATCCTCCCAAAATGCATTGCAGTGCTGAAGGGGAGTGGCTGGTTCCCATCGGGAAATGCA 1414
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Pred. No. 6.9e-104;
0; Mismatches 246;
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; STRANDEDNESS: singl
; TOPOLOGY: linear
US-08-440-815-1
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
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Best Local Sim
Matches 512;
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APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
APPLICATION NUMBER: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOTChia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C1
TELECOMMUNICATION INFORMATION:
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APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: 5.25 inch,
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       416
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                                                         cattcaacctgtactacatggagtctgatgatgatcatggggtgaaatttcgagagcatc 415
                                                                                                                                  tcaagttcactctacgagactgcaatagcattccattggttttaggaacttgcaaggaga 355
                                                                                                                                                                               ATAATTGGCTGTTGACCAGTTGGATCTCTAACGAAGGTGCTTCCAGAATTTTTATTGAAC
                                                                                                                                                                                                     acaattggctgagaacaaactgggtcccccaggaactcagctcagaagatttatgtggagc 295
                                                                                                                                                                                                                                                      ATGAAAACTATCCCCCCATCCACACCTATCAAGTGTGCAAAGTTATGGAACAGAATCAGA
                                                                                                                                                                                                                                                                          atgaacattacacacccatcaggacttaccaggtgtgcaatgtcatggaccacagtcaaa 235
                                                                                                                                                                                                                                                                                                                           TCCGGACCCTTTTGGCCAGCCCCAGTAACGAAGTGAATTTATTGGATTCGCGCACTGTCC 754
                                     CCTTTAACATGTATTATTTTGAGTCGGATGATGAGAATGGGAGAATATCAAAGAGAACC
                                                                                                          TCAAGTTTACTCTGAGGGATTGCAACAGCCTTCCTGGAGGACTGGGGGACTTGCAAGGAGA
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genentech, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 351.4; DB 2;
Pred. No. 6.9e-104;
0; Mismatches 246;
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US-08-673-789-1
                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,81:
APPLICATION NUMBER: 09/177,81:
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPRA: (212) 751-6849
TELEY: 421792
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ZHOU, REN
APPLICANT: T.; KROME
APPLICANT: GEORGE, F
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application Patent No. 5814479
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/673,789
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1415
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STREET: 34
CITY: NEW
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              TYPE: N
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STRANDEDNESS:
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              NUCLEOTIDE
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345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                      USA
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T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
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 DOUBLE
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                   GENERAL INFORMATION:

APPLICANT: Maisonpierre, et a
TITLE OF INVENTION: EHK AND R
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                 Sequence 100, Application Patent No. 5843749
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Query Match 43.0%;
Best Local Similarity 67.1%;
Matches 511; Conservative
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                               cctgcaatgctggctatgaagaaagaggttttatgtgccaa
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                                                                                                                                                                                                                                                                                                                                                                                                    tcaaaaagtgcccatttacagtgaagaatctggctatgtttccagacacggtacc---ca 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tttatttggcatttcaagatgttggtgcttgtgtgtgccttggtgtctgtgagagtatact 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          accgtattctgaagctcaacactgagattagagaagtaggtcctgtcaacaagaagggat 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agtttacaaagattgacaccattgcagctgatgaaagtttcactcaaatggatcttgggg 475
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                                                                                                                                                                                                                                                                            tggactcccagtccctggtggaggttagagggtcttgtgtcaacaattctaaggaggaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITATCTTGCTTTCCAAGATGTCGGTGCTTGCATTGCTCTGGTTTCTGTCCGTGTCTACT 1111
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                                                                                                                    ATCCTCCCAAGATGCATTGCAGTGCTGAAGGGGAGTGGCTGGTTCCCATTGGGAAATGCA 1291
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Pred. No. 2.3e-103;
0; Mismatches 247;
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Regeneron Pharmaceuticals, Inc 7 Old Saw Mill River Road

US/08469537A

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Best Local (
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                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
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FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3592 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: USSN
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version CURRENT APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE
                                                                                                       748
                                                                                                                              139
                                                                                                                                                           889
 868
                                                   808
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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APPLICATION NUMBER: USSN
FILING DATE: 28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                     79 tocaatgaagtcaatctactggattcaaaaacaattcaaggggagctgggctggatctct 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kempler, Ph.D., Gail PREGISTRATION NUMBER: 32,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: USSN 08/406,247 FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                           Local Similarity
les 501; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                      TCCAACCAAGTTGTGTTGCTTGATACATCTACAGTGATGGGAGAACTAGGATGGAAAACA 747
             9tccccaggaactcagctcagaagatttatgtggagctcaagttcactctacgagactgc 318
                                                TATCCACTGAATGGGTGGGATGCCATTACTGAAATGGATGAACACAACAGGCCCATACAT
ATCTCTCGTGATGCTCAGAAAATCTATGTGGAAATGAAGTTCACATTGAGAGATTGT
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/label= N
/note= "Where N =
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Sequence 14, Application US/084490;
Patent No. 5981245;
GENERAL INFORMATION:
APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Like 1
TITLE OF INVENTION: Kinases
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                                                                                                                     REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 14:
MOLECULE
FEATURE:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Angen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                  LENGTH:
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; Sequence 14, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Recepts
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Patent Operation:
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68.28;
Patent Operations/RBW
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Pred. No. 1.1e-101;
0; Mismatches 231;
                                                  Receptor
                                                Protein Tyrosine
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NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: I
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
LOCATION: 34..2994
US-08-702-367A-14
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Matches 509;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CLASSIFICATION: 435
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              ttacagtgaagaatctggctatgtttccagacacggtacccatg--
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TCACAGTCCGCAATCTGGCCCAGTTTCCTGACACCATCACAGGGGCTGATACGTCTTCCC
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                                                       AGGATGTGGGGGCCTGCATCGCCCTGGTATCAGTCCGTGTTCTATAAAAAGTGTCCAC
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Pred. No. 1.1e-101;
0; Mismatches 231;
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LOCATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 509; Conserv
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APPLICANT: FOX, Gary M.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
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MEDIUM TYPE: Floppy
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TYPE: nucleic acid
STRANDEDNESS: Single
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                           caaactgggtccccaggaactcagctcagaagatttatgtggagctcaagttcactctac 310
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       CTGATTGGATCACCCGAGAAGGGGCTCAGAGGGTGTATATTGAGATTAAATTCACCTTGA 349
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                                                                                                                                                                                                                                                                                 Score 344.4; DB 6;
Pred. No. 1.1e-101;
0; Mismatches 231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT//
ETLING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
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                                                                                     APPLICATION NUMBER: US/08/222,616 FILING DATE: 4-APR-1994 CLASSIFICATION: 530
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CITY: South San Francisco
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Goeddel,
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3348 bases
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.4%; Score 344.4; DB 1; Best Local Similarity 68.2%; Pred. No. 1.1e-101; Matches 509; Conservative 0; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 82:
REFERENCE/DOCKET NUMBER: 82:
TELECOMMUICATION: INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
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; STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-34
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PCT-UG95-04228-34
Sequence 34, Application PC/TUS9504228
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3348 bases
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Matthews, William
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TY
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222
APPLICATION NUMBER: 08/222
APPLICATION NUMBER: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,00
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEPAX: 415/952-9881
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gagactgcaatagcattccattggttttaggaacttgcaaggagacattcaacctgtact
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                                                 CTGATTGGATCACCCGAGAAGGGGCTCAGAGGGTGTATATTGAGATTAAATTCACCTTGA 316
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Pred. No. 1.1
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1.1e-101;
nes 231;
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RESULT 14
US-08-449-645A-16
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                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application Patent No. 5981245 GENERAL INFORMATION:
                              TOPOLOGY: 11r
MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: EPH-Lik
TITLE OF INVENTION: Kinases
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CITY: Thousand Oaks
STATE: Callfornia
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 NAME/KEY:
                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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RESULT 15
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                                                                                           Sequence 16, Application Patent No. 5981246 GENERAL INFORMATION:
APPLICANT: Fox, Gary
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Best Local Similarity
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                                     APPLICANT: FOX, GARY M.
TITLE OF INVENTION: EPH-Lik.
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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Amgen Patent Operations/RBW
140 Dehavilland Drive
Isand Oaks
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68.1%;
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Pred. No. 1.3e-101;
0; Mismatches 231;
                                                                             Receptor Protein
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; LENGTH: 4529 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
LOCATION: 186..3182
US-08-702-367A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.4%; Score 344.4; DB 4; Best Local Similarity 68.1%; Pred. No. 1.3e-101; Matches 512; Conservative 0; Mismatches 231;
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                                                                                          CAGGCTACCAGCAAAAAGGAGACACTTGTGAA 1016
                                              GGATGCACTGCAGTGCAGAAGGAGAATGGTTAGTGCCCATTGGAAAATGTATCTGCAAAG 984
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Search completed: May Job time: 4420 sec 15, 2000, 12:05:01

Title: Perfect score:

US-09-104-340-5 813 1 atggattgtcagct

Sequence:

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Run ğ

nucleic

nucleic search, using sw model

Copyright

GenCore version (c) 1993 - 2000

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is the number of results predicted by chance to have a ter than or equal to the score of the result being printed, fived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             coding
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                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 813; Conservative 0
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07-JAN-1993.
19-JUN-1992;
12-JUN-1991;
12-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Key
5'utr
                                                            Claim 6; Fig 1; 58pp; English.

This sequence encodes human eph/elk-like kinase (HEK). HEK is expressed in both pre-B cells and T cell lines and in a number of tumours of human origin, eg. lymphoid tumours LKG3, Lila-1 and JM, and the epithelial tumour HeLa. This receptor-type thymidine kinase (TK) and/or its ligands are useful as agents in modulation of the production and/or function of pre-B, B and T cells. The TK and its analogues have activity in transducing signals or in stimulating cellular responses such as growth and/or differentiation.

Sequence 3132 BP; 888 A; 711 C; 759 G; 774 T;
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Q34513;
24-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3'utr
                                                                                                                                                                                   therapy etc.
Claim 6; Fig 1; 58pp;
                                                                                                                                                                                                          Receptor-type tyrosine kinase reactive with monoclonal antibody III-A4 - is EPH-ELK-like kinase, useful for phosphorylating proteins in modulating pre-B, B and T cell function, in cancer
                                                                                                                                                                                                                                                               (HALL-) HALL INST MEDICAL RES
Boyd AD, Simpson R, Ward LD,
WPI: 93-036373/04.
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T18394
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V90061
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V62177
Q61342
X12997
Q95110
           Score 813; DB 1;
Pred. No. 6.9e-259;
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, Wicks I, Wilkinson
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                       Length 3132;
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Result No.

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SUMMARIES

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Database

N_Geneseq_36:*

Pred. No. is the nu score greater than and is derived by a

Post-processing: Minimum Match 0% Listing first 45

summaries

Minimum Total number Searched

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DB DB

seq

length: 0 length: 1000000

of.

hits satisfying chosen parameters:

311585 seqs, 125096042 residues

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090659;
11-NOV-1995 (first en
Eph-related PTK Cek4.
Cek4; Eph; protein tyr:
prognosis; ss.
Gallus sp.
        W09515375-A.
08-JUN-1995.
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                                         Location/Qualifiers 32. .2980 /*tag= a
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SCC CCC PTT DR PR
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(LJOL-) LA JOLLA CANCER F
PASQUALE EB, Sajjadi FG;
WPI; 95-215256/28.
WPI; 95-215256/28.
P-PSDB; R75711.
Eph-related protein tyroscancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 85-89; 129pp; English.

Probes derived from the EPH-related PTKs Cek4 (Q90659) and Ce (Q90660) were used to isolate novel CDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues, as well as in the adult brain and retina. Sequence 3254 BP; 926 A; 737 C; 796 G; 795 T;
                                        accattgcagctgatgaaagtttcactcaaatggatcttggggaccgtattctgaagctc
                                                                                                                                                                                                                                                                   atggagtctgatgatgatcatggggtgaaatttcgaggagcatcagtttacaaagattgac
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.5e-170;
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Best Local Similarity
Matches 512; Conserv
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17-MAR-1995; US-406247.
26-JUL-1991; US-736559.
28-OCT-1993; US-144992.
06-JUN-1995; US-469537.
(REGE-) RECENERON PHARM INC.
Maisonpierre PC, Masiakowski P
WPI; 99-04484/04.
                                                                                                                                                                                                                                                                                                                                                                                                                          proteins
Claim 5; Fig 22; 194pp; English.
Claim 5; Fig 22; 194pp; English.
The present invention describes nucleic acid molecules ror ....
The present invention described are the corresponding prot ror 2, ehk-1 and ehk-2. Also described are the corresponding prot Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes rat Ehk-1.
Sequence 3906 BP; 1097 A; 876 C; 990 G; 943 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-1999 (first entry)
Rat receptor tyrosine kinase Ehk-1 encor
Receptor tyrosine kinase; Ror-1; Ror-2;
neurotrophin activity; trkB; proto-onco;
binding protein; BDNF; NT-3; diagnosis;
   1050
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11-FEB-1999
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01-DEC-1998
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           accgtattctgaagctcaacactgagattagagaagtaggtcctgtcaacaagaagggat
                                                             agtttacaaagattgacaccattgcagctgatgaaagtttcactcaaatggatcttgggg
                                                                                                             cattcaacctgtactacatggagtctgatgatgatcatggggtgaaatttcgagagcatc
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ACCGGGTCATGAAGCTGAATACGGAGGTCAGAGATGTAGGACCTCTGAGCAAAAAAGGGAT
                                              AGTACATCAAGATCGATACCATTGCTGCTGATGAGAGCTTCACCGAACTTGACCTTGGAG
                                                                                             CCTTTAACATGTATTATTTTGAGTCGGATGATGAGAATGGGGAGAAATATCAAAGAGAACC
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AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in retreatment and diagnosis of neuronal disorders and reatment reatment respectively. As per fragment was used as a probe to isolate the full-length REK7 cDNA from a rat hippocampal cDNA library. A per fragment was used as a probe to isolate the full-length REK7 cDNA from a rat hippocampal cDNA library. An of REK-IgG fusion was used to screen cultured cell lines for surface expression of REK7-binding activity. Primers based on isolated cligands were used to amplify human breast carcinoma BT20 cell cligands were used to amplify human breast carcinoma BT20 cell conna, and an amplified fragment was used to screen a human foetal brain cDNA library, leading to the isolation of AL-1 cDNA (T18897). So Sequence 4165 BP; 1157 A; 907 C; 1035 G; 1066 T;
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26-OCT-1995; U14016.
27-OCT-1994; US-330128.
07-JUN-1995; US-486449.
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P-PSDB; R97853.
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US5814479-A.
29-SEP-1998.
11-JUN-1996; 673789.
04-JAN-1994; US-177812.
11-JUN-1996; US-673789.
(KROM/) KROMER L F.
                                                                                                                                                                                                                                                   Mouse Bsk receptor-like tyrosine kinase cDNA clone. Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neopla. mourodegenerative disease; limbic system neuron regeneration; chromosomal abnormality; degenerative growth; development disorder; viral infection; bacterial infection; Alzheimer's disease; epilepsy schizophrenia; stroke; cerebral ischaemia; ds.
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The present sequence encodes mouse Bsk, which is a receptor-like tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in Bsk nucleic acid probes, which can be used in detecting alterations in the level of Bsk messenger-RNA (mRNA) in biological samples isolated from a mammal afflicted with a disease, such as neurodegenerative diseases or disorders and neoplasms. The nucleic acid sequence can also be delivered into the limbic system of patients with limbic system neurodegenerative disease, disorder or injury, to promote or enhance limbic system neuron regeneration or growth. Such neurodegenerative disease include, chromosomal abnormalities, degenerative growth and development disorders, viral infections, bacterial infections, brain injuries, neoplastic conditions, Alzheimer's disease, epilepsy, schizophrenia, or stroke and cerebral ischaemia.
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Best Local Sim
Matches 511;
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(WOUD/) WOUDE G F V.
(ZHOU/) ZHOU R.
Kromer LF, Schulz NT, NYPI; 98-541751/46.
P-PSDB; W71628.
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                                                        ATAAAAAGTGTCCCTCTGTAGTAAGACACTTGGCTATCTTCCCTGACACTATCACTGGAG
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R 28-OCT-1993; US-144992.
R 06-UUN-1995; US-469537.
R 06-UN-1995; US-469537.
REGENERON PHARM INC.
MAISONDIETTE PC, Maslakowski P PPSDB; W83148
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17-MAR-1995;
26-JUL-1991;
28-OCT-1993;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                            proteins
Claim 7:
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The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding prof Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes rat Ehk-2.

Sequence 3592 BP; 946 A; 916 C; 894 G; 834 T;
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Rattus s
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Rat receptor tyrosine kinase Ehk-2 encoding DNA.
Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2;
neurotrophin activity; trkB; proto-oncogene; tyrosine
binding protein; BDNF; NT-3; diagnosis; ss.
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                                               gtccccaggaactcagctcagaagatttatgtggagctcaagttcactctacgagactgc
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Query Match
Best Local Sin
Matches 509;

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42.48;

Score 344.4; DB 1; Pred. No. 8.3e-104; D; Mismatches 231;

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                                Or prodn.

Claim 1; Page 57-62; 133pp; English.

Claim 1; Page 57-62; 133pp; English.

CDNAs (T02946-49) coding for 4 novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were isolated from a human foetal brain cDNA library using a directed PCR approach with primers (see T02960-61) based on conserved regions of receptor PTKs and EPH-like receptor PTKs. HEK7, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known when the contained contained for prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T02948 standa
T02948;
16-APR-1996
receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. The isolated cDNas are used for prodn. of recombinant HEKs and chimeric receptors, in hybridisation assays, and detect abnormalities in HEK receptor genes.

Sequence 3116 BP; 859 A; 720 C; 812 G; 725 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
Key
                                                                                                                                                                                                                          New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., us diagnostically and therapeutically to modulate receptor activa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPH-like receptor protein tyrosine kinase HEK8 cDNA EPH-like receptor protein tyrosine kinase; PTK; HEK human eph-like kinase; therapy; diagnosis; antibody
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12-OCT-1995; U04228.
04-APR-1995; U04228.
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(GETH ) GENENTECH INC.
Bennett BD, Goeddel D,
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T03100;
14-FEB-1996
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Protein tyrosine-kinase; pTK;
differentiation; ss.
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DR WPI; 95-366160/47.

DR PPSDB; R85936.

PT Agonist antibodies which activate specific protein tyrosine PT Agonist antibodies which activate chimeric proteins of kinase extracellular PT domain and Ig constant domain, useful for studying, and therapeutic PT modulation of, cell growth and differentiation

PS Disclosure; Page 88-92; 125pp; English.

CC DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify novel pTK genes. The bpTKs, CC pTK1, bpTK2, bpTK3, bpTK4, bpTK5 and bpTK7 (R85924-28 and R85935, CC respectively) are expressed in human brain tissue and show homology CC to known pTKs. A full-length sequence for the bpTK7 gene (T03100) cc was obtd. This gene may be used to design new drugs, peptides and cc antisense constructs that modulate pTK activity.

**Cornence 3348 BP; 924 A; 769 C; 855 G; 800 T;
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PT or prodn.

PS Claim 1; Page 66-71; 133pp; English.

CC cDNAs (T02946-49) coding for 4 novel human EPH-like receptor protein CC cDNAs (T02946-49) coding for 4 novel human EPH-like receptor protein CC tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, CC extensive homology to the catalytic domain of chicken EPH-like receptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show CC extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known CC EPH-like receptor. The isolated cDNAs are used for prodn. of recombinant HEKs and chimeric receptors, in hybridisation assays, and CC to detect abnormalities in HEK receptor genes.

SQ Sequence 4529 BP; 1449 A; 834 C; 1000 G; 1246 T;
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P-PSDB; R85092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
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EPH-like receptor protein tyrosine kinase HEK11
EPH-like receptor protein tyrosine kinase; PTK;
human eph-like kinase; therapy; diagnosis; antil
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16-APR-1996
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Jing S, Welcher
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                                                                                                                                                                                               Claim 1; Page 49-54; 133pp; English.

CDNAS (T02946-49) coding for 4 novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were isolated from a human foetal brain cDNA library using a directed PCR approach with primers (see T02960-61) based on conserved regions of receptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cck5, Cck7 and Cck8. HEK11 shows no homology to any known EPH-like receptor. The isolated cDNAs are used for prodn. of recombinant HEKs and chimeric receptors, in hybridisation assays, and
                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
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WPI; 95
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16-APR-1996 (first entry)
                                                                                                                                                                           to detect abnormalities in HEK receptor genes. Sequence 3162 BP; 921 A; 667 C; 775
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W09621013-A1.
11-JUL-1996.
03-JAN-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES F
(SUGE-) SUGEN INC.
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Mouse developmental kinase 1; MDK1 T2; recept Mouse developmental kinase 1; MDK1 T2; recept RTK; signal transduction; probe; diagnosis; neurodegeneration; neuroproliferation; cance
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C. CDNA cloning using adult mouse brains and Northern blotting cidentified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that coded for truncated versions (W03422 and W03423, respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

C. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1 treatment of diseases characterised by abnormal signal transduction. Sequence 2323 BP; 680 A; 497 C; 609 G; 537 T;
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96-333988/33.
            ggatgtactgcagtacagaaggcgaatggcttgtacccattggcaagtgttcctgcaatg
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GAATGCATTGCAGTGCAGAAGGAGAGTGGCTAGTACCCATTGGAAAATGCATCTGCAAAG
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67.3%;
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abnormalities
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Pred. No. 1.1e
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03-JAN-1995; US-368776.
(PLAC) MAX PLANCK GES FO (SUGE) SUGEN INC.
Clossek T, Millauer B,
                                                                                                                                                                                                                                                                      Example 1; Page 111-12; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting identified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that coded for truncated versions (W03422 and W03423; respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1 T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2901 BP; 890 A; 578 C; 650 G; 783 T;
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Mouse developmental kinase 1; MDK1 T1 clone.
Mouse developmental kinase 1; MDK1 T1; rece
RTK; signal transduction; probe; diagnosis;
neurodegeneration; neuroproliferation; canc
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T32961;
11-NOV-1996 (f1:
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caaactgggtccccaggaactcagctcagaagatttatgtggagctcaagttcactctac
                                                        ccatcaggacttaccaggtgtgcaatgtcatggaccacagtcaaaacaattggctgagaa
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                                        CGATAAGAACATACCAGGTGTGCCAGGTCATGGAGCCCAACCAGAACAACTGGCTGCGGA
                                                                                               GGATTTCCTCTCCACCCAGTGGGTGGGAAGAAATTAGTGGTTTGGATGAGAACTACACTC
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233.316
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317.2062
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splicing 2839.2843
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Pred. No. 1.2e-100;
0; Mismatches 237;
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be; diagnosis; gene therapy;
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11-UTL-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES FO (SUGE-) SUGEN INC.
Clossek T, Millauer B,
WPI; 96-33388/33.
P-PSDB; W03421.
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Key
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Mouse developmental kinase 1; MDK1; rec
Mouse developmental kinase 1; MDK1; rec
signal transduction; probe; diagnosis;
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Sequence 4304 BP; 1297 A; 875 C; 1043 G; 1089 T;
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clone (T32960) codes for mouse de
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Query Match
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Cek7', Eph; protein tyrosine
prognosis; ss.
Gallus sp.
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Novel EPH-related PTK CDNA clone Cek7 (given in 090653) and its variant Cek7+ (090661) were isolated from a chick embryo library in lambda gtl1, and another variant, Cek7' (090662), from a chick embryonic brain cDNA library in lambda gtl1. The variants may originate via alternative splicing of the same gene. Cek7 had the lowest level of expression of 7 novel Eph-related kinases examined and was barely detectable in adult tissues.

Sequence 3056 BP; 871 A; 661 C; 762 G; 762 T;
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Q90662;
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P-PSDB; R75714
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                                                                        GCAGATTCCTCGCAGCTGCTAGAAGTGTCAGGCGTCTGTGTCAACCACTCAGTGACTGAT
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tcctgcaatgctggctatgaagaagaggttttatgtgccaa
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5.5e-71;
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08-JUN-1995.
07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RES
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Claim 2; Page 44-47; 129pp; English.
Claim 2; Page 44-47; 129pp; English.
Novel EPH-related PTK CDNA clone Cek7 (given in Q90653) and its
variant Cek7+ (Q90661) were isolated from a chick embryo library in
lambda gtl1, and another variant, Cek7' (Q90662), from a chick
embryonic brain cDNA library in lambda gtl1. The variants may originate
via alternative splicing of the same gene. Cek7 had the lowest level
of expression of 7 novel Eph-related kinases examined and was barely
detectable in adult tissues.
Sequence 3059 BP; 860 A; 632 C; 758 G; 809 T;
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Eph-related PTK Cek7 cDNA.
Cek7; Eph; protein tyrosine-kinase;
prognosis; ss.
Gallus sp.
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WPI; 95-215256/28.
P-PSDB; R75705.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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1 (bases 1 to 3132)

Boyd, A.W., Simpson, R. John, Wicks, I., Method of screening for ligands to a Patent: US 5674691-A 9 07-OCT-1997;
Location/Qualifiers
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Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3149)
Wicks,I.P., Wilkinson,D., Salvaris,E. and Boyd,A.W.
Molecular cloning of HEK, the gene encoding a receptor
kinase expressed by human lymphoid tumor cell lines
proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
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/cell_line="LK63"
/tissue_type="lymphoid tumor"
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BASE COUNT
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TTGDWLNGVRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKAL
ETQSKNCPPVP"

718 711 c 768 9 779 t
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/db_xref="GI:183932"
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Length

3149;

Š 밁 Q 밁 ρy 밁 ρy 밁 Š 밁 δÃ 멍 δÃ 밁 Qy 밁 δÃ В Ş 밁 ρy Query Match Best Local S Matches 813 109 521 581 481 421 461 361 401 301 341 241 281 181 221 121 161 101 61 / Match 100.0%; Local Similarity 100.0%; nes 813; Conservative 0, atggattgtcagctctccatcctccttctcagctgctctgttctcgacagcttcggg gaactgattccgcagccttccaatgaagtcaatctactggattcaaaaacaattcaaggg aagtgcccatttacagtgaagaatctggctatgtttccagacacggtacccatggactcc ttggcatttcaagatgttggtgcttgtgttgccttggtgtctgtgagagtatacttcaaa cattacacacccatcaggacttaccaggtgtgcaatgtcatggaccacagtcaaaacaat gagctgggctggatctcttatccatcacatgggtgggaagagatcagtggtgtggatgaa aacctgtactacatggagtctgatgatgatcatggggtgaaatttcgagagcatcagttt ttcactctacgagactgcaatagcattccattggttttaggaacttgcaaggagacattc **AACCTGTACTACATGGAGTCTGATGATGATCATGGGGTGAAATTTCGAGAGCATCAGTTT** TTCACTCTACGAGACTGCAATAGCATTCCATTGGTTTTAGGAACTTGCAAGGAGACATTC 0; Score 813; DB 9; Pred. No. 4.3e-241; Mismatches 0; Indels 0 Gaps 660 600 640 540 480 420 460 340 280 180 120 160 580 520 360 400 300 240 220 60 0

ORIGIN

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Rattus norvegicus eph-related
(Rek4) mRNA, complete cds.
U69278 U69278.1 GI:1943913
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L1,Y.Y., MCTLernan,C.F. and Feldman,A.M.
Direct Submission
Submitted (01-SEP-1996) Cardiology, University of Pittsbur Lothrop Street, Pittsburgh, PA 15213, USA
On Apr 18, 1997 this sequence version replaced gi:1698721.
Location/Qualifiers
1. 3077
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Eutheria; Rodentia; Sciurognathi; Muridae; Murin
1 (bases 1 to 3077)
Li,Y.Y., McTiernan,C.F. and Feldman,A.M.
II-1 beta alters the expression of the receptor
gene r-EphA3 in neonatal rat cardiomyocytes
and J. Physiol. 274 (1), H331-H341 (1998)
877
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LETTOSKRGDEVDX
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35. .2989
LETQSKNGPVPV"
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/codon_start=1
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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RESULT 5
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bp mRNA receptor ty

tyrosine

kinase

(Mek4)

secreted

mRNA,

complete cds. M68515 M68515.1 GI:4 MUSMEK4SE Mouse eph-

KEYWORDS SOURCE ACCESSION VERSION

receptor tyrosine kinase. Mus musculus (strain IRC

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Swiss Webster) 11.5

day embryo embryo

GI:454828

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           gctggctatgaagaaagaggttttatgtgccaa
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                                                 aggatgtactgcagtacagaaggcgaatggcttgtacccattggcaagtgttcctgcaat
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Sajjadi,F.G., Pasquale,E.B. and Subramani,S. Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
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LKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKCPFTVKNLAMFPDTVPMD
SQSLVEVRGSCYNNSKEEDPPRNYCSTEGEWLVPIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPPHSSTQEDGSMNCRCENNYFRAEKDPSMACARPPSAPRNVISN
INETSVLLDWSWPLDTGGRKDIFNIICKKCGNNYRQCEPCSPW7RFLPRQLGITNTT
VTVTDLLAHTNYTFEIDAVNGVSELSSPPRQYAAVSITTNQAAPSPWTIKDRTSRN
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Sajjadi,F.G., Pasquale,E.B. and Subramani,S.
Identification of a new eph-related receptor ty
from mouse and chicken that is developmentally
encodes at least two forms of the receptor
New Biol. 3, 769-778 (1991)
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IRLEGVYTKSKEEMIVTEYMENGSLDSFLKKHDAGTFVLQLVGKLRGLASGMKYLSDM
GYVHRDLAARNILLNSNLVCKVSDFGLSRVLEDDPEAAYTTRGGKIPIRWTSPEAMSY
RKFTSASDVWSYGIVLWEYMSYGERPYSOMSNODVIKAVDEXRLDPPMDCPAALYQL
MLDCWOKDRNMRPKFEQLVSILDKLIRNFGSKKIITSAADERSHLLDOSNODIATEH
TTGDWLNGMRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISIKAL
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New Biol. 3, 769-778 (1991)
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M68514.1 GI:454809
receptor tyrosine kinase.
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/db_xref="taxon:9031"
/dev_stage-"10 day embryo"
/tissue_type="embryo"
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/product="receptor tyrosine
/protein_id="AAA48666.1"
/db_xref="G1:211447"
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Sequence
I15007
I15007.1
                                                                                                       Unclassified.

1 (bases 1 to 3254)

Pasquale, E.B. and Sajjadi, F.G.

Eph-related tyrosine kinases, nucleotide
                                                                                            Patent:
                      Conservative
                                                            t: US 5457048-A 15 10-OCT-1995;
Location/Qualifiers
1. 3254/
/organism="unknown"
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                   Ohta,K., Nakamu.....
Ando,M. and Tanaka,H.
The receptor tyrosine kinase,
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subtypes of motoneurons in Mech. Dev. 54 (1), 59-69 (196404128
                                                                                                   D38174.1 GI:1236732 receptor tyrosine kinase; Gallus gallus spinal cord Gallus gallus
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                                     ATTCCCCGCGAGGGGCTCAGAGGGTATATATTGAAATCAAGTTCACGCTGAGAGACTGC
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Direct Submission

Submitted (09-SEP-1994) to the DDBJ/EMBL/GenBank databases.

Kunimasa Ohta, Kumamoto University Graduate School of Medical Sciences, Dept. of Neuroscience and Immunology; 4-24-1 Kuhonji, Kumamoto, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
3 (bases 1
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/db_xref="taxon:9031"
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0; Mismatches 252;
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U58332
U58332.1 GI:
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Submitted (14-MAY-1996) Pathology & Laboratory Medicine,
of Pennsylvania, 36th and Hamilton Walk, Philadelphia, PA
                                                                                                                                                                                                                                                                                                                                       Lee, A.M., Navarratnam, D., Ichimiya, S., Greene, M.I. and Davis, J.G. Cloning of m-ehk2 from the murine inner ear, an eph family receptyrosine kinase expressed in the developing and adult cochlea DNA Cell Biol. 15 (10), 817-825 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3943)
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                                                                                                                                        /organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
285. .3392
/product="receptor tyrosine kinase"
/protein_id="AAB53836.1"
/db_xref="G1:1457961"
/translation="MGGCEVREFLLOFGFFLPLLTAWTGDCSHVSNQVVLLDTTTVMG
ELGWKTYPLNGWDAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVE
                                                                                        /note="eph-related tyrosine kinase; simil norvegicus receptor-like tyrosine kinase Accession Number S51605"
                                                                             /codon_start=1
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GCTGATGGGGATTGGCTTGTTCCTCTTGGAAGGTGTATCTGCAGTACAGGGTATGAAGAA
                               acagaaggcgaatggcttgtacccattggcaagtgttcctgcaatgctggctatgaagaa 795
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DWASQUSLALSWQAPAFSKAILDYETKY EKEHEQLTYSSTRAKAPSVIVTGLKPAT
TYIEHIRVRTATQYSGYSGYSOKTEETGDETSDMAAEQGGILVIATAAVGGFTLLVILTL
FFLITGRCQWYIKAKMKSEKRRTHLQNGHLRFPGIKTVIDPDTYEDPSLAVHEFAKE
LDPSRIRIERVLGAGEFGEVCSGRLKTPGKREIPVAIKTLKGGAPHPVTAGGSLPPRI
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DAWSYGIVMEVMSSTDKLKTRUSSALTILVEDILVMPESSPGDVPEYPLEVYGGMLDSG
DAWSYGIVMEVMSVGERPYMEMSNQDVILSIEEGYRLPSGAFPSLQALMLGWGK
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KKGQYKSNFMAAGFTTFDLISRMSIDDIRRIGVILIGHQRRIVSSIQTLRLHMMHIQE
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Direct Submission
Submitted (07-APR-1994) G.C. Miescher, Neurological Clinic & Submitted (07-APR-1994) G.C. Miescher, Neurological Clinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research Dept., University Hospitals Basel, 4031 Basel, SWITZERI 3 (bases 1 to 3531)
Maisoppierre,P.C., Barrezueta,N.X. and Yancopoulos,G.D.
Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 3531)

Taylor, V., Miescher, G.C., Pfarr, S., Honegger, P., Breitschopf, Lassmann, H. and Steck, A.J.
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                      /Translation-"MRGSGPRADADGPRAQASWCHARRGDTPRVPASLAGCYSAPLK
GPLWTCLLLCAALTILLASPSNEVNLLDSRTYLGDLGWIAFPKNGWEEIGEVDENYAP
IHTYQVCKVMEQONGNUNLLISWISHEVNLLDSRTYLGDLGWIAFPKNGWEEIGEVDENYAP
IHTYQVCKVMEQONGNUNLLISWISHEVNLTGEIFTEVENCOPLSKKGFY
LAFQDVGACIALVSVRYYYKKCPSVVRHLAVFPDTITGADSSQLLEVSGSCVVHSYTD
DPPKMHCSAEGEWLVPJGKCKKAGYEEKNGTCQVCRPGFFRASPHSQTCSKCPPHSY
THEEASTSCVCEKDYFRRESDPPTMACTTPSPVTNVKKGKIAKNSISLSWQEPDRPNG
IILEYEIKYFERDQETSYIIKSKETTITAEGLKPASYVYFQIRARTAAGVVFSRRE
EFETTPVFAASNDQSQIPIIAVSVTVGVILLAVMIGFLLSGSCCECGCGRASSLCAVA
HPSLIWRCGYSKAKQDPEEEKMHFHNGHIKLDGVRTYIDPHTYEDPTQAVHEFAKEIE
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/product="receptor tyrosine kinase"
/protein_id="cAA55357.1"
/db_xref="GI:531544"
/db_xref="SWISS-PROT:P54757"
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{	t ASCITIERVIGAGEFGEVCSGRLKLPGKRELPVAIKTLKVGYTEKQRRDFLSEASIMG}
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PAALYQLMLDCWQKDRNSRPKFDDIVNMLDKLIRNPSSLKTLVNASSRVSTLLAEHGS
LGSGAYRSVGEWLEAIKMGRYTEIFMENGYSSMDAVAQVTLE"
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Pred. No. 5.7e-98;
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Maisomplerre,P.C., Masiakowski,P. and
Ehk and Ror tyrosine kinases
Patent: US 5843749-A 102 01-DEC-1998;
Location/Qualifiers
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Pred. No. 5.8e-98;
0; Mismatches 246;
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Sequence 1 :
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Caras, I.W. and Winslow, J.W.
AL-1 neurotrophic factor antibodies
Patent: US 5798448-A 1 25-AUG-1998;
Location/Qualifiers
1. 4165
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M.musculus mRNA for ty
X65138 S51422
X65138.1 GI:54083
Sek gene; Tyrosine kii
Gilardi-Hebenstreit, P., Nieto, M.A., Frain, M., Chestier, A., Wilkinson, D.G. and Charnay, P. An Eph-related receptor protein tyrosine kina:
                                                                 Direct Submission
Submitted (26-MAR-1992) P
de Genetique Moleculaire,
                                                                                                         Charnay,
                                                                                                                               Eukaryota; Metazoa;
Rodentia; Sciurognat
                                                                                                                                                           Mus musculus
                                                                                                                                                                       house mouse.
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                                                     FRANCE
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nilarity 66.5%;
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LKTTRVSITDLLAHTNYTEEIRANNGVSKYNESPDOSVSVTVTINQARESSIALVQAK
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                                                                                                                                                                      GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 127779) from the original journal article. This sequence comes from Fig. 5.
*ERRATUM* Gilard: Hebenstreit et al., Oncogene (1992)7, 2499-2:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        Gilardi-Hebenstreit, P., Nieto, M.A., Frain, M., MB Chestler, A., Wilkinson, D.G. and Charnay, P. An Eph-related receptor protein tyrosine kinase expressed in the developing mouse hindbrain Oncogene 8 (4), 1103 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.

Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

1 (bases 1 to 4242)
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Query Match 43.2
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Matches 535; Conservative
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                          GATGTGGGTGCTTGCATCGCCCTGGTGTCTGTCTGTCTACAAGAAGTGTCCACTC
                                              aacactgagattagagaagtaggtcctgtcaacaagaagggattttattttggcatttcaa
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                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Tarvaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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AW230735 uo67c05.y
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AF116297 Armillari
AA952881 on76f10.s
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AA93650 ok63f04.s
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Contact: Wilson
                                                                                                                                  Homo sapiens
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 2663
High quality sequence stops: 276
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2663
Std Error: 0.00
Seg primer: M13Rev
Eukaryota; Metazoa; Chordata; Craniata; Verto
Eutheria; Primates; Catarrhini; Hominidae; HC
1 (bases 1 to 427)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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/db_xref="GDB:3847311"
/db_xref="Taxon:9606"
/clone_1ib="Soares retina N2b4HR"
/clone_1ib="Soares retina N2b4HR"
/sex="male"
/clone_1ib="Soares retina N2b4HR"
/sex="male"
/clone_1ib="Soares retina N2b4HR"
/sex="male"
/clone_1ib="Soares retina N2b4HR"
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/clone_1ib="Soares
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 bp mRNA EST 12-MAR-1998 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1469977 3' gb:M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);, m
                                                                                                                                             Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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Large-scale Sequencing Analysis of Unpublished (1998)
On May 8, 1995 this sequence vers. Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Suwon, Kyunggido, Korea
                                                                                                                                               1 (bases 1 to 225)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                         AA752361
96GS0872 Rice
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43; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On Jan 14, 1998 this sequence version replaced g1:1798438
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                               Oryza sativa
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h quality sequence stop: 373.
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0872 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
020ne 96GS0872, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1469977"
/clone_lib="NCI_CGAP_GC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
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67.2%;
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Pred. No. 33;
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Library construction: Natalia S. Akopyants, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain V1 genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
                                                                                                                                                                                                                                                                                             Unpublished (1999)
On Mar 23, 1999 this sequence version
Other_GSSs: lm30b08.x1
Other_GSSs: Sylvanian No. 188
                                                                                                                                                                                                                                                                                                                                                                                                 Akopyants, N.S., Beverley, S.M., Clifton, S., Marra, M., Hillier, L., Chinwalla, A., Pape, D., Martin, J., Wylie, T., Blistain, A., Schmitt, A., Person, B., Theisin, R., Ritter, E., Ronko, T., Schmitt, A., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                 Contact: Akopyants, NS / Beverley, SM WashU Leishmania Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ850374 407 bp DNA GSS 15-OCT-1999 LMAJFV1_lm30b08.yl Leishmania major FV1 random genomic library Leishmania major genomic clone LMAJFV1_lm30b08 5', genomic sur
                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                              WashU Leishmania Project
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                                                                                                                                                   Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa"
/cultivar="Milyang23"
/db_xref="taxon:4530"
/clone="96GS0872"
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Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 77;
0; Mismatches
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                                                                                                                                                                                                                   Louis, MO 63108, USA
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AU033295/c
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AU033295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D. (beverley@borcim.wustl.edu)
Seq primer: -40RP from Gibco
Class: shotgun
                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:1900162.
                                                                                                                                                                                                                                                                                          Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 392)
Yamamoto,K. and Sasaki,T.
Rice cDNA from etiolated shoot
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa.
Oryza sativa
                                                                                                                                                                                               Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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46; Conservative
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Location/Qualifiers
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                                                                                                                                                           tsasak1@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Clone_lib="Leishmania major FV1 random genomic library"
/lab_host="ToP10 (Invitrogen)"
/note="Vector: p2ero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For
this library, DNA was sheared to give a tight size
distribution of 1-1.5kb fragments, blunt-ended with T4 DNA
polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into p2ero-2 vector's EcoRV site."
a 148 c 107 g 90 t
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Rice shoot Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Leishmania major"
/strain="Friedlin strain VI"
/db_xref="taxon:5664"
/clone="LMAJFVI_lm30b08"
/clone="S6421_1A"
/clone_11b="Rice shoot"
/note="Etiolated shoot (8
                                                         /organism-"Oryza sativa"
/strain-"Nipponbare, sub_species Japonica"
/db_xref-"taxon:4530"
                                                                                                                                       Location/Qualifiers
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Pred. No. 1.1e+02;
0; Mismatches 29;
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1A, mRNA
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Best Local Similarity
Matches 48; Conserv
Query Match
Best Local Similarity
Matches 43; Conserv
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Unpublished (1999)
On Jun 5, 1998 this s
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, I., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagama, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y., Yoshino, M., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                            Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
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    Conservative
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                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="1700040E03"
                                                                                                                                                                           /clone_lib="Mus musculus adult C57BL/6J testis"
/sex="male"
                                                                                                                                                                                                                                                     organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                              /dev_stage="adult"
96 c 62 g
                                                                                                                                                    /tissue_type="testis"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                  32.2%;
63.2%;
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  <u>,,</u>
Score 28; DB 50;
Pred. No. 1.4e+02;
0; Mismatches 25
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Pred. No. 1.3e+02;
0; Mismatches 34
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C57BL/6J testis Mus
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AV393461/c
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AW230735/c
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        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 518)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                    AW230735 518 bp mrna EST 10-DEC-1999 u067c05.y1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:2647592 5' similar to gb:D21089 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (HUMAN); mRNA sequence.

AW230735 TEGERAL AW230735 TEGERAL AW230735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 473)
Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S.
A Large Scale Structural Analysis of cDNAs in a Unicellular Green Alga, Chlamydomonas reinhardtii. I. Generation of 3433
Non-redundant Expressed Sequence Tags
DNA Res. 6, 369-373 (1999)
On Jul 9, 1999 this sequence version replaced gi:5434219.
Contact: Yasukazu Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV393461 473 bp mRNA EST 21-JAN-2000 AV393461 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii CDNA clone CL07e07_r, mRNA sequence.
AV393461 GI:6547677 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
                                                                                                                                       AW230735.1 GI:6560031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydomonas reinhardtii
                                                                                                          house mouse.
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Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="CL07e07_r"
/clone_lib="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Chlamydomonas
/strain="C9"
/db_xref="taxon:3055"
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On May 18, 1998 tl
Contact: Chie Owa
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                                          RIKEN
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Carninci,p., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Akahira,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsayama,T., Niitsuma,H., Oda,J., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV153845 307 bp mRNA EST AV153845 Mus musculus hippocampus C57BL/6J clone 2900058C14, mRNA sequence. AV153845
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Tissue Procurement: Glibert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing C
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On Jul 9, 1999 this sequence version replaced g1:5434208.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                        Genome Science Laboratory
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40; Conservative
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1 Koyadai, Tsukuba,
81-298-36-9145
81-298-36-9098
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a 116 c 163 g 68 t 2 others
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/dev_stage="3 months, virgin"
/lab_host="DH10B"
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/clone="IMAGE:2647592"
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/strain="FVB/N"
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Armillaria gallica
Eukaryota; Fungi; Basidiomycota;
Tricholomataceae; Armillaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF116297 291 bp Dr
Armillaria gallica strain
AF116297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                          Direct Submission
Submitted (23-DEC-1998) Biology, University of Toronto at
Mississauga, 3359 Mississauga Road, Mississauga, Ontario L5L
                                                                                                                                                                                                                                                                                                          2 (bases 1 to 291)
Anderson, J.B. and Hodnett, B.
                                                                                                                                                                                                                                                                                                                                        Michigan hardwood forest
Unpublished
                                                                                                                                                                                                                                                                                                                                                                        Random nuclear DNA sequences
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42; Conservative
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2900058C14"
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                                                                                                                                                                                   /organism="Armillaria gallica"
/strain="C33r"
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75 c 80 g
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94 c 72 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mus musculus hippocampus C57BL/6J adult"
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L.8e+02;
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zs89h08.rl |
similar to '
AA282730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Jan 17, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA952881 329 bp mRNA EST on76f10.sl Soares_NFL_T_GBC_S1 Homo sapiens IMAGE:1562635 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                              77
                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1562635"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
          402 bp mRNA EST 13-AUG-1997 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704703 TR:G1049078 G1049078 SRP30C. ;, mRNA sequence.
                                                                                                                                      247
                                                                                                                                                                                                                                                                                         31.7%;
                                                                                                                                                                                                                                                                       Score 27.6; D
Pred. No. 1.9e
0; Mismatches
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                                                                                                                                                                                                                                                                       ; DB 40;
1.9e+02;
nes 29;
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CDNA clone
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RESULT 1
AI869632
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AUTHORS
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Best Local S
Matches 45
                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                  281 TCGACCATCCCACTCCATCCTTCTGCACATCAGCATAACAGACATCCCCAGCTTCTCGC 222
                                                                                                                                                                                                                                                                                                 221 ATGTGATCCCTCAG 208
                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       2 tggattgtcagctctccatcctccttctcagctgctctgttctcgacagcttcgggg 61
                                                                                                                                                                                                                                                                                                                                  aactgattccgcag 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
On May 8, 1995 this sequence version replaced gi:800900. Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1150
Email: Robert_Strausberg@nih.gov
                                                                                                                                                      mRNA sequence.
AI869632
                                                                                                                                                                       AI869632 419 bp mxna
w199d07.x1 NCI_CGAP_Brn25 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LINL; contact the IMAGE Consortium (infedimage.llnl.gov) for further information. Insert Length: 960 Std Error: 0.00 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 419)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                              Homo sapiens
                                                                                                                                   AI869632.1 GI:5543600
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1 (bases 1 to 402)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:5854427"
/db_xref="taxon:9606"
/clone="IMAGE:704703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_GCB1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 31;
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JOURNAL
COMMENT
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AUTHORS
TITLE
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AI992021
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 tctccatcctccttctctcagctgctctgttctcgacagcttcggggaactgattccgc 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 agccttccaatgaa 87
                                                                                                                                                                                                                                                                                                                                                                                                                   AGGCCTCGGAGCAA 253
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 484)

NCI/NINDS-CGAP http://www.ncbi.nim.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)

On Dec 20, 1995 this sequence version replaced gi:1133839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
On Jun 72, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                         AI992021 484 bp mRNA EST ws44b02.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                         AI992021.1 GI:5838926
                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

131 c 104 g 88 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/clone="IMAGE:2433037"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27.6; DB 61;
Pred. No. 2e+02;
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IMAGE:2500011 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosenfeld
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SOURCE
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                  JOURNAL
                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGCCTCGGAGCAA 247
                                                                                                                                                                                  Fugu rubripes.

Fugu rubripes

Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygil;

Eukaryota; Metazoa; Chordata; Vertebrata; Acanthopterygil; Percomorpha;

Neopterygil; Teleostel; Euteleostel; Acanthopterygil; Percomorpha;

Tetraodontiformes; Tetraodontoidel; Tetraodontidae; Fugu.

1 (bases 1 to 549)

Cmith S. Meek, S., Warner, S., Umrania, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome

Clone distribution: NCI-CGAP clone distribution

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                    Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk Vector: pBluescript II KS
                                                                                                                                                    Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                         AL012136
AL012136.1 GI:2677569
GSS; genome survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -40UP from Gibco High quality sequence stop: 471. Location/Qualifiers
sequence
                                                                        V_type: phagemid
                                                                                                                                                                                                                                                                                                                                                                                   F.rubripes GSS sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
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              pass dye-terminator sequencing of cosmid cloned genomic
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/clone="IMAGE:2500011"
/clone_11b="NCI_CGAP_Brn25"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                         549 bp
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Pred. No. 2.1e+02;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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                                                                                                                                                                                                                                                                                                                                                                                   genomic survey sequence.
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COMMENT

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BASE COUNT
ORIGIN
                                                                                                FEATURES
                                                                                source
             169
          /organism="Fugu rubripes"
/db_xref="taxon:3103"
/clone_lib="cosmid 027G17"
/clone="027G17aG10"
a 131 c 98 g 140 t
                                                                                           Location/Qualifiers
             11
             others
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                                                              Query Match
Best Local :
                                                   Matches
                                                Local Similarity 67.2
nes 39; Conservative
  82
              9 tcagctctccatccttcttctcagctgctctgttctcgacagcttcggggaactg
TCAGCTGTGCTTCCTCCACCTTCAGCAGTGCTGGGTTTTTTGCCTGCTTACGGGTCCTG
                                                             31.78;
                                                Score 27.6; DB 82
Pred. No. 2.2e+02;
0; Mismatches 19
                                                   19;
                                                  Indels
                                                                       Length 549;
                                                  0
                                                Gaps
                         66
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0

Search completed: May Job time: 19138 sec 15, 2000, 11:20:15

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Database :
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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Perfect score:
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seq
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length: 1000000
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87
1 atggattgtcagct
            Pending_Patents_NA:*
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-160.230 Million cell updates/sec
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Cgn2_6/ptodata/2/pna/US081B_COMB.seq: *
(cgn2_6/ptodata/2/pna/US081B_COMB.seq: *
(cgn2_6/ptodata/2/pna/US081D_COMB.seq: *
(cgn2_6/ptodata/2/pna/US081D_COMB.seq: *
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(cgn2_6/ptodata/2/pna/US082B_COMB.seq: *
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(cgn2_6/ptodata/2/pna/US084B_COMB.seq: *
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(cgn2_6/ptodata/2/pna/US087B_COMB.seq: *
(cgn2_6/ptodata/2/pna/US088B_COMB.seq: *
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(cgn2_6/ptodata/2/pna/US089B_COMB.seq: *
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(cgn2_6/ptodata/2/pna/US089G_COMB.seq: *
(cgn2_6/ptodata/2/pna/US089G_COMB.seq: *
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(cgn2_6/ptodata/2/pna/US08G_COMB.seq: *
(cgn2_6/ptodata/2/pna/US08G_COMB.seq: *
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/cgn2_6/ptodata/2/pna/US081/
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/cgn2_6/ptodata/2/pna/US06_COMB.seq:*
/cgn2_6/ptodata/2/pna/US07_COMB.seq:*
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45 / cgnn2_6/ptodata/2/pna/US092C_COMB.seq; *
46 / cgnn2_6/ptodata/2/pna/US092C_COMB.seq; *
47 / cgnn2_6/ptodata/2/pna/US092C_COMB.seq; *
48 / cgnn2_6/ptodata/2/pna/US092C_COMB.seq; *
59 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
50 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
51 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
52 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
53 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
54 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
55 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
56 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
57 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
58 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
59 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
61 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
62 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
63 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
64 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
65 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
66 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
67 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
68 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
69 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
69 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
69 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
60 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
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66 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
67 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
68 / cgnn2_6/ptodata/2/pna/US093C_COMB.seq; *
69 / cgnn2_6/ptodata/2/pna/US09AC_COMB.seq; *
69 / cgnn2_6/ptodata/2/pna/US09AC_COMB.seq; *
69 / cgnn2_6/ptodata/2/pna/US09AC_COMB.seq; *
69 / cgnn2_6/ptodata/2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 321	Result No.
87 87 31	Score
100.0 100.0 35.6	% Query Match
87 813 453	% Query Match Length DB ID
40 40 92	Ħ
87 40 US-09-104-340-6 813 40 US-09-104-340-5 453 92 US-60-172-375-1200	
Sequence 6, Appli Sequence 5, Appli Sequence 1200, Ap	Description

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SEQ ID NO 6

LENGTH: 87

TYPE: DNA

CORGANISM: Homo sapiens

FEATURE:

NAME/KEY: exon

LOCATION: (1)..(87)

OTHER INFORMATION: Exon I
US-09-104-340-6
                                                                                                                                   Sequence 6, Application US/09104340

GENERAL INFORMATION:
APPLICANT: BOYD, Andrew W
APPLICANT: BOYD, Andrew W
APPLICANT: LACKMANN, MAITIN
TITLE OF INVENTION: RECEPTOR-LIGAND SYSTEM AND ASSAY
FILE REFERENCE: boydug
CURRENT APPLICATION NUMBER: US/09/104,340
CURRENT APPLICATION NUMBER: P07549
EARLIER APPLICATION NUMBER: P07549
EARLIER FILING DATE: 1997-06-25
NUMBER OF SEG ID NOS: 25
NUMBER OF SEG ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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                 I of HEK gene
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0 US-60-133-875-1293
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0 US-60-168-139-6260
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0 US-60-144-084-19436
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0 US-60-150-522-250
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0 US-60-165-277-2955
0 US-60-173-383-144401
0 US-60-167-217-13894
0 US-60-167-217-13894
0 US-60-168-359-997
0 US-60-168-359-997
0 US-60-160-190-651
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24606, A
Sequence 1293, Ap
Sequence 1243, Ap
Sequence 2003, Ap
Sequence 2003, Ap
Sequence 2006, Ap
Sequence 6260, Ap
Sequence 6260, Ap
Sequence 17798, A
Sequence 17798, A
Sequence 19436, A
Sequence 19784, Ap
Sequence 3508, Ap
Sequence 5570, Ap
Sequence 5570, Ap
Sequence 22118, Ap
Sequence 22118, Ap
Sequence 19357, A
Sequence 5923, Ap
Sequence 11278, A
Sequence 11278, A
Sequence 11278, A
Sequence 11278, A
Sequence 11400, A
Sequence 11278, A
Sequence 11400, A
Sequence 11400, A
Sequence 11400, A
Sequence 11278, A
Sequence 11400, A
Sequence 214, App
Sequence 214, App
Sequence 11478, A
Sequence 11478, A
Sequence 21478, A
Sequence 21478, A
Sequence 21478, Ap
Sequence 11478, A
Sequence 21478, Ap
Sequence 514, App
Sequence 651, App
Sequence 564, App
```

```
APPLICANT: BOYD, Andrew W
APPLICANT: BOYD, ANDREW W
APPLICANT: BOYD, MITCHIA
APPLICANT: LACKMANN, Martin
ITILE OF INVENTION: RECEPTOR-LIGAND SYSTEM AND ASS
FILE REFERENCE: boydug
CURRENT APPLICATION NUMBER: US/09/104,340
CURRENT FILING DATE: 1998-06-25
EARLIER APPLICATION NUMBER: PO7549
EARLIER FILING DATE: 1997-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 6
SEQ ID NO 6
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: (1)..(813)
OTHER INFORMATION: Exons I, II and III of HEK gen
US-09-104-340-5
                                                                       RESULT 3
US-60-172-375-1200/c
US-60-172-375-1200/c
Sequence 1200, Application US/60172375
GENERAL INFORMATION:
APPLICANT: Schuch, Wolfgang
APPLICANT: Ceder, David
APPLICANT: O'Neill, John M.
APPLICANT: O'Neill, John M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM WHEAT CARYOPSIS
FILE REFERENCE: PL-0051 P
CURRENT APPLICATION NUMBER: US/60/172,375
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 11151
SOFTWARE: PERL Program
SEQ ID NO 1200
LENGTH: 453
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US-09-104-340-5
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Best Local Similarity 100.0%;
Matches 87; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09104340 GENERAL INFORMATION:
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Best Local Similarity
Matches 87; Conserv
                               TYPE: DNA ORGANISM: Triticum aestivum FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Inc
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Pred. No. 3.8
0; Mismatches
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Pred.
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No. 2.7e-16;
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US-60-185-359-1293 Application US/60185359

Sequence 1293, Application US/60185359

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

ITILE OF INVENTION: The Drosophila Genome, Primary Nucleic

TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid

ITILE OF INVENTION: Sequences and Uses Thereof

FILE REFERENCE: CL000284

CURRENT APPLICATION NUMBER: US/60/185,359

CURRENT FILING DATE: 2000-02-28

NUMBER OF SEQ ID NOS: 2926

SEQ ID NO 1293

SEQ ID NO 1293

LENGTH: 263456
; TYPE: DNA
; ORGANISM: Drosophila
US-60-185-359-1293
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; LOCATION: 82, 192, 271, 409
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-375-1200
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; ORGANISM: Drosophila
US-60-164-769-24606
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US-60-164-769-24606
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Best Local S
Matches 49
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CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 27328
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 24606
LENGTH: 120625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24606, Application US/60164769
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
TITLE OF INVENTION: Acid Sequences, Systems Containin the I
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: CL000144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 AGTGATTCATCGACCTGTCA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 GGATACTAAGGCAGCCATGTTCATGCCTCCCAGCTGTTCTGTTATCAACAAACTGNTGAT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 totocatcotoctcottotcagotgototgttotogacagotttogggggaactgattocgc 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 actgattccgcagccttcca 82
                                                                                                                                                                                                                                                                                                                                                                                                                                              74 agcc 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ggattgtcagctctccatcctccttctcagctgctctgttctcgacagcttcgggga 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28.8; DB 30,
Pred. No. 1.3e+02;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Systems Containin the Nucleic Acid Sequences
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13;
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CURRENT APPLICATION NUMBER: US/60/133,875
CURRENT FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 2916
SOFTWARE: PERL PROGRAM
SEQ ID NO 1443
LENGTH: 310
TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-528-237-1293

Sequence 1293, Application US/09528237

Sequence 1193, Application US/09528237

SERVAL INFORMATION:

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic

TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic acid;

TITLE OF INVENTION: Sequences and Uses Thereof

FILE REFERENCE: CL000284

CURRENT APPLICATION NUMBER: US/09/528,237

CURRENT ETLING DATE: 2000-03-17
                                                        ; OTHER INFORMATION: US-60-133-875-1443
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; ORGANISM: Drosophila
US-09-528-237-1293
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1293
LENGTH: 263456
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Best Local Similarity
 Query Match
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                                                                                                       FEATURE:
NAME/KEY: unsure
LOCATION: 2, 16, 119
OTHER INFORMATION: a (
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Garrow, Bonnie L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Goralski, Thomas J.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM RAT LIVER
FILE REFERENCE: PZ-0118 P
                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 totocatoctcotcottotcagotgototgttotogacagottogggggaactgattocgc 73
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 32.98;
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Pred. No. 1.5e+02;
0; Mismatches 22;
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 Score 28
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Pred. No. 1.5e+02;
0; Mismatches 22;
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                                                                                                                 unknown,
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83;
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Length 310;

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RESULT 10
US-09-514-000-369/c
; Sequence 369, Application US/09514000
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US-60-168-139-2003
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US-09-514-000-6818/c
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US-09-514-000-6818
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GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequence And Uses Thereof
FILE REFERENCE: 38-21(15490)A
CURRENT APPLICATION NUMBER: US/60/168,139
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 3432
SEQ ID NO 2003
LENGTH: 4266
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GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15490)
CURRENT APPLICATION NUMBER: US/09/514,000
CURRENT FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 15034
SEQ ID NO 6818
LENGTH: 999
TYPE: DNA
SECONETION OF SECONETIC 
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Best Local Similarity
Matches 47; Conserv
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Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                                                                                                                                                                      610 gattacgggctcaccttcctcggcctgctcggcatcgccattcccaacttcatgctggca 669
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                                                                                                                                                                                                                                       64 ctgattccgcagccttcc 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 ctgattccgcagccttcc 81
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                                                                                                                                                                                                                                                                                                                                             4 gattgtcagctctccatcctccttctcagctgctctgttctcgacagcttcggggaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            totocatcotcottotcagotgototgttotogagottoggggaactgattocg
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                                                                                                                                                                        ctgatcctgatgtatttc 687
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0; Mismatches
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28.4; DB 91;
Pred. No. 1.1e+02;
0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Best Local Similarity
"~+~hes 42; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: unsure at all n locations
US-60-164-320-6260
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: Sequence 6260, Application US/60164320
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                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-60-183-791-6260/c
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15490)B CURRENT APPLICATION NUMBER: US/09/514,000
CURRENT FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 15034
SEQ ID NO 369
LENGTH: 38536
TYPE: DNA
CONTROL TO A 
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SEQ ID NO 6260
LENGTH: 1454
TYPE: DNA
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GENERAL INFORMATION:
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Best Local Similarity
Matches 47; Conser
APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthemonas campestris Genome
FILE REFERENCE: 38-10(15804)B
CURRENT APPLICATION NUMBER: US/80/183,791
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 6260
                                                                                                                                                                                                                                                                                   Sequence 6260, Application US/60183791 GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthomonas campestris Genome
FILE REFERENCE: 38-10(15804)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/60/164,320 CURRENT FILING DATE: 1999-11-10
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Pred. No. 1.1e+02;
0; Mismatches 23;
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Pred. No. 1.
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1.5e+02;
hes 31;
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Best Local Similarity 77.3
Matches 34; Conservative
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Best Local Similarity
Matches 42; Conserv
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APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15761)B
CURRENT APPLICATION NUMBER: US/09/531,113
CURRENT FILING DATE: 2000-03-22
CURRENT FILING DATE: 10620
NUMBER OF SEQ
SEQ ID NO 16459
          APPLICANT: Byrum, Joseph R.
APPLICANT: Coombs, Brian E.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Nelson, Donald E.
APPLICANT: Nelson, Donald E.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 38-21 (15444) B
FILE REFERENCE: 38-21 (15444) B
CURRENT APPLICATION NUMBER: US/60/144,084
CURRENT FILING DATE: 1999-07-16
RUMBER OF SEQ ID NOS: 47776
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EQ ID NO 33845
LENGTH: 174
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                                                                                                                                                                                                                                                                              INFORMATION
                                                                                                                                                                                                                                         Buehler, Robert E.
                                                                                                                                                                                                                                                           Abad, Mark S.
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Pred. No.
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Pred.
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ed. No. 1.1e+02;
Mismatches 23;
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89;
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; TYPE: DNA;
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3109-014-Q1-K1-A10
US-60-144-084-16459
                                                                                                                                                                                                                 SEQ ID NO 17798

LENGTH: 391

TYPE: DNA

ORGANISM: Glycine max

FEATURE:
FOTHER INFORMATION: Clone ID: LIB3109-053-Q1-K1-D9
US-60-144-084-17798
Search completed: May 13, Job time: 5212 sec
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Best Local Similarity 77.3
Matches 34; Conservative
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Best Local Similarity 77.3
Matches 34; Conservative
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APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 38-21 (15444)B
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/60/144,084
CURRENT FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 47776
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Byrum, Joseph R.
Coombs, Brian E.
Heck, Gregory R.
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Shukla, Hridayabhiramjam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomas J.
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77.3%;
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                                                                                                                                     Score 28; DB 86;
Pred. No. 1e+02;
0; Mismatches 10;
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Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                        Score
      Issued_Patents_NA:*

1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
6: /cgn2_6/ptodata/
7: /cgn2_6/ptodata/
      Query
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87
1 atggattgtcagct
                                                                                                                                                                                                                                                                                                                                        Match
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107.646 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                        Length
    DB
   5438126-1
US-08-619-542B-36
US-08-619-542B-37
US-08-901-200A-14
US-07-980-364B-13
US-07-981-703-10
US-07-991-703-28
US-08-147-023-28
US-08-147-023-28
US-08-147-023-29
US-08-155-343A-20
US-08-49-656-77-29
US-08-49-553A-20
US-08-49-570-28
US-08-49-653-70
US-08-49-653-20
US-08-49-653-20
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US-08-715-106-9
US-08-619-542B-34
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Sequence 9, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 36, Appl
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 28, Appli
Sequence 20, Appli
Sequence 7, Appli
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Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 28, Appli
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US-08-167-919A-9
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25	25.2	25.2	25.2	5	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2
28.7	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29:0
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Sequence 1, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 5, Appli	Sequence 7, Appli	Sequence 20, Appl	Sequence 5, Appli	-	Sequence 20, Appl	`	•	Sequence 20, Appl	Sequence 28, Appl				

ALIGNMENTS

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nucleic acid	••	RISTICS:		TELEX: 230 901 SANS UR	TELEFAX: (516) 742-4366	TELEPHONE: (516) 742-4343	ATION INFORMAT	REFERENCE/DOCKET NUMBER: 9159	REGISTRATION NUMBER: 31,346	NAME: DiGiglio, Frank S.	Y/AGENT INFORMATION		ATION NO	TIC	FILING DATE: 12-DEC-1991	- 20	H	ING DATE:	APPLICATION NUMBER: PK6841 (AU)	PRIOR APPLICATION DATA:	¥	R-1994	APPLICATION NUMBER: US/08/167,919A	LICATION DATA:	PatentIn	OPERATING SYSTEM: PC-DOS/MS-DOS	COMPUTER: IBM PC compatible	TYPE: F1	笳	530	ĸ	••	Garden City	00 Garden City Plaza		DENCE ADDRESS	R OF SEQUENCES: 14	OF INVENTION: AND USE THEREOF	NVENTION: A	Wilkin	Ward, I		Simpson, Ric	APPLICANT: Boyd, Andrew W.	AL IN	5674691	Sequence 9, Application US/08167919A	US-08-167-919A-9

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US-08-715-106-9
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Best Local Similarity 100.0%;
Matches 87; Conservative (
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                                TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No. 6020306
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                               NAME: DIGIGIO, Frank S. 146
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 91:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                           APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pair
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: A NOVEL TITLE OF INVENTION: AND USE NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: SI
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Boyd, Andrew WAPPLICANT: Simpson, Richa APPLICANT: Wicks, Ian APPLICANT: Ward, Larry D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 GAACTGATTCCGCAGCCTTCCAATGAA 186
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08 FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilkinson, David
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100..3048
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Pred. No. 4.6e-21;
); Mismatches 0;
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US-08-619-542B-34
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Best Local Similarity 100.0%;
Matches 87; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/08619542B Patent No. 5830662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: The Trustee:
APPLICANT: of New York
                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 324 base pairs
                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,542B
FILING DATE: June 21, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFERMATION:
                                                                                                                                                                                                  NAME: White, John P.
REGISTARION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
                                                FEATURE:
                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GAACTGATTCCGCAGCCTTCCAATGAA 186
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                              NAME/KEY:
                                                                              TOPOLOGY:
                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                     TELEFAX: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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100..3048
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                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                             linear
                                                             peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHOD FOR CONSTRUCTION OF NORMALIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunham LLP
of the Americas
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Pred. No. 4.6e-21;
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Query Match
Best Local Similarity
Matches 38; Conserv

Conservative

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Indels

0

Gaps

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31.3%;

Score 27.2; DB Pred. No. 0.6; 0; Mismatches

BB

Length 324;

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RESULT 4
5438126-1/
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US-08-619-542B-36/c
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APPLICANT: DEGROOT,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36, Application US/08619542B Patent No. 5830662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 03-FEB-1992
                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1594 CCTTCCCCTACCTTCTGAGAGGATGGGGTCCTGGGAACTGCAGGACACAGCTCCCCCAGC 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 405,342
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1534 CTCCCA 1529
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The Trustees of Columbia University in the City APPLICANT: of New York TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORWALIZED TITLE OF INVENTION: CDNA LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/
FILING DATE: June 21, 1996
CLASSIFICATION: 435
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                                                    TELEFAX:
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                                                    (212)
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                                                                                                        42840-A-PCT-US
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Query Match
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""+ches 37; Conserve
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                                                                                                                Query Match
Best Local
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FILING DATE: June 21, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 323 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: The Trustees of Columbia University in the City APPLICANT: of New York
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62 aactgattccgcagccttcc 81
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TOPOLOGY: lir
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LOCATION:
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                                                           TCGATGCCCACCTCCTCATAATCCTTCTCCAGGGCAGCCATATCCTCACGGGCCTCGGAG 216
                                                                                                 1 Similarity
46; Conserv
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1185 Avenue of the Americas
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                                                                                                 Conservative
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                                                                                                Score 25.6; DE Pred. No. 2.1; 0; Mismatches
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Pred. No. 2.1;
0; Mismatches
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Best Local (
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                                                               Matches
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C.
NAME: MEYERS, THOMAS C.
ODD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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APPLICANT:
                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 466..930
OTHER INFORMATION:
                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 204..393
OTHER INFORMATION:
                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 1..950
                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
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                                                            1 Similarity 57.7
45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
DEDNESS: single
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OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
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                                                                           29.0%;
                                                                                                                                                /note= "hOP-2 genomic sequence"
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                                                          Score 25.2; D
Pred. No. 4.2;
0; Mismatches
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Query Match
Best Local Similarity
"~+~hes 45; Conserve
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; LOCATION:
US-07-800-364B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony J.
TITLE OF INVENTION: Bone and Cartilage Inductive Proteins
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: «
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                    POSITION IN UNITS: b
                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
   LIBRARY: Human heart cDNA library stratagene catalog
   LIBRARY: #936208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1003 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617-876-1170
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LOCATION:
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                                                                                                                                                           LOCATION:
                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                   CLONE:
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TISSUE TYPE: Human Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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Conservative

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Mismatches

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29.0%; 57.7%;

Score 25.2; Pred. No. 4

DB 1; Length 1003;

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RESULT 9
US-07-989-847-11
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Query Match
Best Local Similarity
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[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                          CLONE: hH38
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617-876-1170
                                                                                                      FEATURE:
                                                                                                                                   FEATURE:
NAME/KEY:
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LIBRARY: Human heart cDNA library stratagene catalog
LIBRARY: #936208
                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Israel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMBER OF SEQUENCES:
                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 GGTCCAGGAGCAGTCCAA 165
                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                 ORGANISM: H
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1003 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kapinos, Ellen J
REGISTRATION NUMBER: 32
                                                                                                                    LOCATION:
                                                                                                                                                                                                             UNITS:
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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    Legal Affairs, Genetics Institute, Inc
87 CambridgePark Drive

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                                                                        mRNA
1..997
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                                                                                                                    mat_peptide
427..843
                                                                                                                                                                                                                                                                                                 Human Heart
                                                                                                                                                                                                                                                                                                                                                            cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Bone Morphogenetic Protein Heterodimers, Compositions and Methods of Use.
 29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    11:
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Score 25.2; DB Pred. No. 4.3;
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             Length 1003;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
              FILING DATE: 20-AUG-
PRIOR APPLICATION DATA:
                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                              FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 6: FILING DATE: 04-DEC-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 1
FILING DATE: 28-JAN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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APPLICATION NUMBER: US 8
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWI'
STREET: 53 STATE STREET
                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                 FILING DATE: 21-NOV-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER
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                                                           PRIOR APPLICATION DATA:
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                                                                                                                       APPLICATION NUMBER: US 5 FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                           APPLICATION NUMBER: US 579,865 FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: UFILING DATE: 19920221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 02109
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                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
APPLICATION NUMBER:
                                             APPLICATION NUMBER:
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TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MASSACHUSETTS
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RUEGER, DAVID C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OZKAYNAK, ENGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                          22-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                US 621,849
                                                                                                                                                                                                                                                                                                                           US 621,988
                                                                                                                                                                                                                                                                                                                                                                                                                       US 827,052
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                                              US 569,920
                                                                                                                                     US 599,543
                                                                                                                                                                                     US 600,024
                                                                                                                                                                                                                                   US 616,374
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US 483,913
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 422,613 FILING DATE: 17-OCT-1989

APPLICATION NUMBER:

US 315,342

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US-07-901-703-10
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Best Local :
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                                                                                                                                                                                                                                                                                                                                    Patent No. 5344654
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/07901703 Patent No. 5344654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23-FEB-1989
PRIOR APPLICATION NUMBER: US 232,630
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: EXCHANGE PLACE, 53 STATE STREET
                                                                                                                                                                                                        TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED TITLE OF INVENTION: OSTEOGENIC PROPERTIES NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                              APPLICANT: RUEGER, DAVID C
APPLICANT: KUBERAŞAMPATH, T
APPLICANT: OPPERMANN, HERMI
APPLICANT: OZAKAYNAK, ENGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INAME/KEY: CDS
LOCATION: 490..1696
OTHER INFORMATION: /f
OTHER INFORMATION: /F
OTHER INFORMATION: /r
                                                                                                               STREET: BOSTON
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Local Similarity 57.7%;
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STRANDEDNESS: Single
                                                                         COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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OZAKAYNAK, ENGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function= "OSTEOGENIC PROTEIN"
/product= "hOP2-PP"
/note= "hOP2 (cDNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27,829
                                                                                                                                                                                                                                                                                                 THANGAVEL
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NAME/KEY: CDS
LOCATION: 490..1696
COTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "hop2-pp"
OTHER INFORMATION: /note= "hop2 (cDNA)"
US-07-901-703-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.0%;
Best Local Similarity 57.7%;
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: OPPERM
APPLICANT: OZKAYN
APPLICANT: KUBERA
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SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: ci
ORIGINAL SOURCE:
ORGANISM: Homo
TISSUE TYPE: H.
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/901,703
FILING DATE: 19920616
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: mrcm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 gattccgcagccttccaa 83
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CITY: BOSTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
                                                   APPLICATION NUMBER: US/08/147,023 FILING DATE: 21-FEB-1992
                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                           STATE:
 APPLICATION NUMBER:
                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 ttgtcagctctccatcctccttctcagctgctctgttctcgacagcttcggggaact 65
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5468845
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                                                                                                                                                                                                                                                                            53 STATE STREET
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OZKAYNAK, ENGIN
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RUEGER, DAVID C.
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E: HIPPOCAMPUS
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                                                                                                                                                                                                                                                                                               HURWITZ & THIBEAULT
US 810,560
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FILING DATE: 20-DEC-1991 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 8: FILING DATE: 28-JAN-1992

US 827,052

FILING DATE: 22-FEB-PRIOR APPLICATION DATA:

US 621,988

APPLICATION NUMBER: US 660,162 FILING DATE: 22-FEB-1991

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Query Match
Best Local Similarity
"~+~hes 45; Conserve
                                                                                                      ; OTHER INF
US-08-147-023-28
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 2:
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 483,913 FILING DATE: 22-FEB-1990 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 621,849 FILING DATE: 04-DEC-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                    LOCATION: 490..1696
OTHER INFORMATION: /:
OTHER INFORMATION: //
OTHER INFORMATION: //
                                                                                                                                                                                                                                                                                                         LENGTH: 1723 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CRI
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FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: PITCHER, EDMUND REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 179,460 FILING DATE: 08-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 616,374 FILING DATE: 21-NOV-1990
                                                                                                                                                                                                                       TISSUE TYPE: HIPPOCAMPUS
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                                                                                                                                                                                        NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                           LENGTH:
                 Conservative
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                             linear
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                                29.0%;
57.7%;
                                                                                                                  /function= "OSTEOGENIC PROTEIN"
/product= "hOP2-PP"
/note= "hOP2 (cDNA)"
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              Score 25.2; DI
Pred. No. 5.1;
0; Mismatches
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                                              DB 1;
                33;
                                              Length 1723;
              Indels
              0
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-206-864-3
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US-08-206-864-3
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                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
APPLICATION NUMBER: US 07/
FILING DATE: 21-FEB-1192
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
PEGISTRATION NUMBER: 27 82
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                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: OPPERMANN, HERD
APPLICANT: OZKAYNAK, ENGII
APPLICANT: KUBERASAMPATH,
                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: RECOMBINANT OSTEOGENIC PROTEIN PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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ZIP: 01748
                                                                  NAME/KEY:
LOCATION:
                                                                                                                    ORGANISM: Homo sapiens
TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                               TELEFAX:
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JONES, WILLIAM K
TUCKER, RONALD F
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OZKAYNAK, ENGIN
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            /function= "OSTEOGENIC PROTEIN"
/product= "hOP2-PP"
/note= "hOP2 (cDNA)"
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Local Similarity 57.7 hes 45; Conservative

57.7%;

Pred. No. 5.1; 0; Mismatches

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                                                                                                                                 Query Match
Best Local Similarity
Matches 45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICANT:
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NAME: PITCHER Esq., EDMUND R.
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION: (508) 435-9001
                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
                                                                  933
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                                                                                                                                                                                                                                                                                                    LENGTH: 1723 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 490..1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/278,729A FILING DATE: 20-JUL-1994
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GGTCCAGGAGCAGTCCAA 1010
                               gattccgcagccttccaa 83
                                                                TTACAAGGTGCCCAGCATCCACCTGCTCAACAGGACCCTCCACGTCAGCATGTTCCAGGT 992
                                                                                           ttgtcagctctccatcctcctccttctcagctgctctgttctcgacagcttcggggaact 65
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OZKAYNAK, ENGIN
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                                                                                                                                   Conservative
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                                                                                                                                 Score 25.2; DB Pred. No. 5.1; 0; Mismatches
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; NAME/KEY: CDS
; LOCATION: 490..1696
; OTHER INFORMATION: /f
; OTHER INFORMATION: /p
; OTHER INFORMATION: /n
US-08-480-528a-7
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                                                                                                                    Query Match
Best Local Similarity
Watches 45; Conserve
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                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,528A
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                  933
 993
                         66 gattccgcagccttccaa 83
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                                                                                       6 ttgtcagctctccatcctccttctcagctgctctgttctcgacagcttcgggggaact 65
                                                                  TTACAAGGTGCCCAGCATCCACCTGCTCAACAGGACCCTCCACGTCAGCATGTTCCAGGT 992
GGTCCAGGAGCAGTCCAA 1010
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VENTION: OP3-INDUCED MORPHOGENESIS
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KUBERASAMPATH,
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                                                                                                                                                      29.0%;
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                                                                                                                                                                                                                                      /function= "OSTEOGENIC PROTEIN"
/product= "hOP2-PP"
/note= "hOP2 cDNA"
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                                                                                                                                  Score 25.2; D
Pred. No. 5.1;
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Search completed: May 15, 2000, 12:05:03 Job time: 4422 sec

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US-09-104-340-6 87

Run

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Copyright

GenCore version (c) 1993 - 2000

Scoring table:

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length: length:

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Total number of hits satisfying chosen parameters:

311585 segs, 125096042 residues

Searched:

Database

N_Geneseq_36:*

Post-processing: Minimum Match 0% Listing first 45

summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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21-JUN-1991; AU-006841.
12-DEC-1991; AU-009992.
(HALL-) HALL INST MEDICAL RE:
Boyd AD, Simpson R, Ward Li
WPI; 93-036373/04.
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                                          This sequence encodes human eph/elk-like kinase (HEK). HEK is expressed in both pre-B cells and T cell lines and in a number of tumours of human origin, eg. lymphoid tumours LK63, Lila-1 and JM, and the epithelial tumour HeLa. This receptor-type thymidine kinase (TK) and/or its ligands are useful as agents in modulation of the production and/or function of pre-B, B and T cells. The TK and its analogues have activity in transducing signals or in stimulating cellular responses such as growth and/or differentiation.

Sequence 3132 BP; 888 A; 711 C; 759 G; 774 T;
                                                                                                                                                                                                                                                                  WO9300425-A.
07-JAN-1993.
19-JUN-1992;
21-JUN-1991;
12-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Key
                                                                                                                                                       therapy etc.
Claim 6; Fig 1; 58pp;
                                                                                                                                                                              Receptor-type tyrosine kinase reactive with monoclonal antibody III-A4 - is EPH-ELK-like kinase, useful for phosphorylating proteins in modulating pre-B, B and T cell function, in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                      signal_peptide
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24-MAY-1993
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100. .3051
/*tag= b
3052. .313;
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/note= "Potential transmembrane region"
160. .216
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/note=
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Human glial tumour
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C-Delta-1 gene (al
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Tumor necrosis fac
TNF-R1-D ligand p
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Result No.

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Query Match

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SUMMARIES

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Q34513 Q347542 V777542 V21209 V84466 Q981466 Q9814663 T94563 T94563 T94564 Q41564 Q41564 Q48737 Q38946 Q38735 Q388735 Q388735 Q388735 Q388735

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Query Match 100.0%; Best Local Similarity 100.0%; Matches 87; Conservative 0;

Score 87; DB 1; Le Pred. No. 3.9e-19; Pred. No. 3.9e-19;

Length 3132; Indels

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Gaps

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Q56233 Q55917 Q67313 Q45118 Q451426 Q77106 Q77106 Q77206 Q77208 T73208 T

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                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT A plant ferritin gene induced in acidic soil - derived from Acacia
PT plants, improves resistance to acidic growth conditions
PS Claim 1; Page 6-7; 9pp; Japanese.
CC This sequence represents a plant ferritin gene. The plant ferritin
CC gene, whose production is induced in acidic soil, is involved in the
CC coccurrence of disorders in a plant caused by acidic soil as well as
CC in improvements in the resistance of a plant to acidic conditions.
CC This gene can be used for breeding of plants highly resistant to acidic
CC soil. The cDNA or its fragment can also be used for diagnosis of a
CC plant planted in acidic soil by determining the expression of ferritin
CC in it. Ferritin can be expressed excessively by introducing the cDNA
CC of the invention into a plant in the sense direction to reinforce the
CC resistance of the plant to acidic soil. Therefore acidic soil which could
CC not be utilised for agricultural purposes can be utilised by the
                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 41
  V57542 standard;
V57542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resulting plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NETT-) NETTAI RIN SAISEI GIJUTSU KENKYU KUMIAI.
WPI; 97-344897/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1995; JP-323527.
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1079. .1088
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248. .874
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1055. .105
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/note= "PolyA_site"
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V21209_09/c
                                                                                                                                                                                                                                                                                                                                                                                                                        Newly identified calcium channel sub:units alpha II and alpha IH

for development of cell lines which express the novel calcium

reproper channels, useful for screening channel (ant)agonists

Claim 2; Pages 26-33; 45pp; English.

This represents a cDNA from BAC bk206c7 encoding a partial sequence of a

chuman calcium channel subunit alpha-1. The invention provides isolated

chuman calcium channel subunit alpha-1. The invention provides isolated

chuman calcium channel subunit alpha-1 and

claim 1: An eukaryotic cell transiently or stably transformed with an

claim 2: Expression vector containing the calcium subunits encoding DNA fragments

can be used for expressing the calcium channel. The cells are optionally

further transformed to express alpha 2 delta or beta calcium channel or

compounds capable of acting as agonists or antagonists for the alpha-II

calcium channel. The nucleic acid sequences can be used in histological

assay to determine the tissue distribution of the novel calcium channel
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 35
                    WO9838301-A1.
03-SEP-1998; CA0173.
27-FEB-1998; US-030482.
25-FEB-1998; US-039204.
(REUR-) NEUROMED TECHNOLOGIES I
Baillie DL, Snutch TP;
WPI; 98-481203/41.
                                                                                                                                                                                                                                                                                              5258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human calcium channel subunit alpha-1 partial sequence encoding cDNA Calcium channel subunit alpha-1; recombinant; alpha 2 delta; beta calcium channel; agonist; antagonist; alpha-1I calcium channel; histological assay; tissue distribution; ds.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                         Name
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Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foetal deficiency; blood; allergy; renal; ds;

inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

cognitive disorder; schizophrenia, prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid digestion;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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Brewer LA, Carter KC, Dillon PJ, Ebner R, Endres Fan P, Feng P, Ferrie AM, Fischer CL, Florence C Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben Shi Y, Seppet DR, Wei Y, Young P, Yu G, Zeng Z; WPI; 99-059865/05.
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Query Match Best Local S Matches 44

44; Conservative

29.98;

Score 26; DB Pred. No. 11; 0; Mismatches

DB 11;

1; 30;

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11-SEP-1989; US-405342.
03-FEB-1992; US-830766.
(ARCH-) ARCH DEV CORP.
Degroot LJ. Nakai A;
WPI; 95-274923/36.
P-PSDB; R78318.
                                                                                                  Human secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; inflammation; ischaemic shock; Alzheimer; disease; restenceis; lymphoma; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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Q95110 encodes R78318 human thyroid hormone receptor alpha-1 (hT alpha-1). The nucleic acid can be used to develop prods. for use analysis assays and therapeutic agents. hTR-alpha-1 can be used tests for thyroid function, or for producing antibodies for use affinity purificn., detection and quantification.
Sequence 1893 BP; 461 A; 531 C; 551 G; 350 T;
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Human thyroid hormone receptor alpha-1 cDNA.

Human; thyroid hormone; receptor; alpha-1; hTR-alpha-1; analysis; assays; therapeutic agents; antibodies; affinity purification; detection; quantification; ss.
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AC T97
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Best Local S
Matches 37
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30-MAY-1997; US-04bJ.

30-MAY-1997; US-054804.

05-AUG-1997; US-054804.

(HUMA-) HUMAN GENOME SCI INC.

(HUMA-) HUMAN GENOME SCI INC.

TM, Hu JS, Lafleur DW, Moore PA

TM, Hu JS, Lafleur DW, Moore PA

TM, Shi Y, Young P;
                                                              Homo sapiens.
Key
CDS
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30 - MAY-1997
21 - MAR-1997
21 - MAR-1997
21 - MAR-1997
21 - MAR-1997
30 - MAY-1997
30 - MAY-1997
30 - MAY-1997
                                                                                                                                                inhibitor; ss.
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                                                                                                                                                                                                                                                                                           T94563 standard;
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30-MAY-1997;
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1997; US-048069
1997; US-048095
1997; US-048095
1997; US-048096
1997; US-048131
1997; US-048135
1997; US-048166
1997; US-048186
1997; US-048186
1997; US-048186
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d long chain DNA novel
chain DNA; antibody; ne
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                                                        Location/Qualifiers
1. .1269
  /product=
                                   /*tag=
                                                                                                                                                                                                                                                                                           DNA;
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                                                                                                                                                                                                                                                                                           1269
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"long chain DNA protein"
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W, Moore PA, Ni J, Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25.6; D
Pred. No. 9.9;
1; Mismatches
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                                                                                                                                                                           nervous
                                                                                                                                                                                                   gene.
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                                                                                                                                                                     disorder; detection;
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Matches 44
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Best Local S
Matches 44
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03-APR-1996; JP-081304.
(ASAH) ASAHI KASEI KOGYO K
KATO C, Takada Y;
WPI; 97-503103/46.
P-PSDB; W32797.
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03-APR-1996; JP-081304,
(ASAH ) ASAHI KASEI KOGYO K
KATO C, Takada Y;
WPI; 97-503103/46.
                                                                                                        Human long chain DNA and antibodies which bind to the peptide(s) - is potentially useful in treating nervous disorders Claim 4; Page 92-93; 109pp; Japanese.

The present sequence represents human derived long chain DNA comprising at least a peptide-encoding region. Peptides encoded by the human derived long chain DNA, may be used for detecting substances which bind to the peptides, and for detecting substances which suppress or inhibit binding to these peptides. The peptides and their inhibitors are potentially useful in treating nervous disorders.

Sequence 1562 BP; 318 A; 506 C; 389 G; 349 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human long chain DNA and antibodies which bind to the peptide(s) - is potentially useful in treating nervous disorders Claim 3; Page 91-92; 109pp; Japanese.

The present sequence represents human derived long chain DNA comprising at least a peptide-encoding region. Peptides encoded by the human derived long chain DNA, may be used for detecting substances which bind to the peptides, and for detecting substances which suppress or inhibit binding to these peptides. The peptides and their inhibitors are potentially useful in treating nervous disorders.

Sequence 1269 BP; 263 A; 413 C; 285 G; 308 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1998 (first entry)
Human derived long chain DNA novel gene.
Human; long chain DNA; antibody; nervous disorder; detection;
inhibitor; ss.
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T94564;
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cagctctccatcctcctcctctcagctgctctgttctcgacagcttcggggaactgatt 69
                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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                                           l Similarity
44; Conser
                                            Conservative
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168. .1439
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/product= "long chain DNA protein"
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                                                       29.2%;
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                                         ; Score 25.4; D; Pred. No. 16; 0; Mismatches
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Pred. No. 15;
0; Mismatches
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88

TTACAAGGTGCCCAGCATCCACCTGCTCAACAGGACCCTCCACGTCAGCATGTTCCAGGT 147 ttgtcagctctccatcctcctcctcagctgctctgttctcgacagcttcgggggaact 65

σ

Matches

Similarity 57. 45; Conservative

0,:

33;

0

Gaps

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                                                                      Problement the control of the process of the sequence is that encoding the human bone morphogenetic protein CC BMP-8. It may be used in the product of a recombinant heterodimeric CC protein having bone stimulating activity. This heterodimer is CC encoded by a sequence encoding BMP-2 or BMP-4 or a fragment and a CC sequence encoding a second protein or fragment, BMP-8. It may be CC used in compsns. for wound healing, tissue repair, and in similar CC compsns. which have been indicated for the use of individual BMPs. CC Increased potency of the heterodimer over individual BMPs may permit CC induces cartilage and/or bone growth in circumstances where bone CC induces cartilage and/or bone growth in circumstances where bone CC fractures and cartilage defects in humans and other animals. The CC contributes to the repair of congenital, trauma induced or oncologic cresection induced craniofacial defects, and also is useful in cosmetic plastic surgery. It may be used in the treatment of periodontal CC disease and in other tooth repair processes. It may also be useful in the transplantation and treatment of conditions exhibiting a decrease in neuronal survival and be useful in the transplantation and treatment of conditions exhibiting a decrease in neuronal survival. It may be useful in the transplantation and treatment CC combined with other agents beneficial to the bone and/or cartilage defect, wound or tissue in question, e.g. EGF, PDGEF, TGF-alpha, CC TGF-beta and insulin-like growth factor

Sequence 1002 BP; 196 A; 330 C; 285 G; 191 T;
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Best Local
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Q41296;
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02-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant hetero-dimeric BMP proteins - are useful in bone defects, healing bone injury and in wound healing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        induction; ss.
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US-787496.
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427. .843
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1. .997
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8. .850
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                29.0%;
57.7%;
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osteoporosis; burns; incisions; ulcers;
ease; fracture reduction; cartilage growth;
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Score 25.2; E
Pred. No. 17;
0; Mismatches
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                              Length 1002;
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GGTCCAGGAGCAGTCCAA 165 gattccgcagccttccaa

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Best Local S
Matches 45
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Mature hOP2 is one of the preferred known morphogens which can be used in the manufacture of pharmaceuticals for inducing non-chondrogenic mammalian tissue growth, progenitor cell proliferation and hepatic tissue growth and for maintaining the phenotypic expression of differentiated cells in a mammal. Morphogenic compositions of the invention can also be used to treat blood disorders and impaired or lost immune function. Morphogens sharing at least 70% homology with hOP2 are included.

Sequence 1723 BP; 265 A; 624 C; 576 G; 258 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q28737
Q28737;
                                                                                                                                                                                              Human osteogenic protein 2 (hop-2) gene.

Bone; loss; increase; fracture; post-menopausal; senile;

osteoporosis; hyperparathyroidism; skeletal microstructure defects;

chronic renal failure; kidney disease; osteomalacia, vitamin D;

deficiency induced osteoporosis, paget's disease;

bon many induced osteoporosis; paget's disease;
                                                                                                                                                                                                                                                                           21-JUL-1993 (first entry)
Human osteogenic protein 2 (hop-
Bone; loss; increase; fracture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compsns. for increasing progenitor morphogen to induce proliferation, neoplastic growth, inducing tissue
W09305751-A
                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                         Q38946
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                                                                                                                                                     bone mass;
phosphate;
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1991; US-667274.
CREATIVE BIOMOLECULES INC.
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                                                                                                                                                     metabolism;
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                                                                          Location/Qualifiers
490. .1696
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Pred. No. 19;
0; Mismatches
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useful for inhibiting
repair and in diagnos
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Best Local
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28-AUG-1991; US-752764.

30-AUG-1991; US-752857.

30-AUG-1991; US-752861.

30-AUG-1991; US-752861.

31-JUL-1992; US-923780.

(CREAT) CREATIVE BIOMOLECULES INC.
COhen CM, KUBETASSAMPATH T, OPPERMANN H,
Pang RHL, Rueger DC, Smart JE;
WPI; 93-117208/14.
                                                                            WO9304692-A.
18-MAR-1993;
28-AUG-1992;
U07358.
30-AUG-1991; US-752764.
30-AUG-1991; US-752861.
30-AUG-1991; US-753059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteopenia or osteoporosis, postmenopausal or senile osteoporosis, hyperparathyroidism and Paget's disease. The methods can be used for hyperparathyroidism at risk for loss of bone mass such as postmenopausal females, aged individuals and individuals undergoing dialysis. The loss of bone mass may result from an imbalance in bone resorption or bone formation, an imbalance of calcium or phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that encoding human osteogenic protein 2 (hOP-2) a morphogenically active protein which may be used as part of a method for treating a bone fracture and a disease which causes or results in bone fractures or other defects in skeletal microstructure. Such diseases include chronic renal failure and other kidney diseases, osteomalacia, vitamin D deficiency-induced
                         Cohen CM, Kuberasampath T, Pang RHL, Rueger DC, Smart WPI; 93-100652/12.
                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                   morphogenic; osteogenic protein; developmental cascade; hOP-2;
inflammation; anti-inflammatory; Transforming Growth Factor;
TGF-beta super-family; hippocampus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of morphogenic or in-vivo morphogenic-stimulating agent - to prevent bone loss or increase, used for treating bone fractures,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                post-menopausal or senile osteoporosis,
Disclosure; Page 115-117; 162pp; Englis
Morphogen-induced modulation of inflammatory response -
             P-PSDB; R33410
                                                   Cohen CM,
                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                             Human OP-2.
                                                                                                                                                                                                                                                                                                                                                    Q38735 standard; cDNA; 1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolism,
                                                                 (CREA-) CREATIVE BIOMOLECULES INC
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mes 45; Conserv
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1279.
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Pred. No. 19;
0; Mismatches
                                                    Oppermann
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                                                    Ozkaynak
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                                                                                                                                                                PT Screening cpds: to determine ability to modulate effective concn.

PT of a morphogen - by assaying test tissue type cells for parameter indicative of a prodn. Level change of morphogen

PT indicative of a prodn. Level change of morphogen

PS Disclosure; Page 95-97; 132pp; English.

CC This sequence encodes the human morphogen hop2, isolated from the CC hippocampus. This morphogen is inactive when reduced but is active CC as an oxidised homodimer and when oxidised in combination with other CC morphogens. These morphogens are capable of stimulating proliferation CC of progenitor cell, stimulating the differentiation of progenitor cells, stimulating the proliferation of differentiated cells and CC supporting the growth and maintenance of differentiated cells, These morphogens may also be capable of inducing redifferentiation of CC committed cells under appropriate environmental conditions.

Sequence 1723 BP; 270 A; 624 C; 572 G; 257 T;
                                                                                             Query Match
Best Local S
Matches 45
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Best Local S
Matches 45
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28-AUG-1992;
30-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morphogen; homodimer; stimulate; proliferation; progenitor cell; differentiation; growth; redifferentiation; transformation; humanise: Drosophila; Xenopus; committed cells; hippocampus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resulting tissue damage, e.g. in autoimmune diseases, diabetes, asthma, ischemia reperfusion injury, etc.
Claim 26; Page 119-121; 165pp; English.
Human osteogenic protein (OP)-2 is a preferred morphogen for use in treating tissue damage in e.g. inflammatory disease, autoimmune disease, arthritis, psoriasis, dermatitis, diabetes and emphysema.

Proteins having at least 70% homology with OP-2 amino acid sequences can also be used. See R33400 for mature hOP-2.
Sequence 1723 BP; 266 A; 625 C; 574 G; 258 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rueger DC, Kuberasampath
WPT or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CREA-) CREATIVE BIOMOLECULES INC. Cohen CN, Kuberasampath T, Oppermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q38859 standard; DNA; 1723
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                            TTACAAGGTGCCCAGCATCCACCTGCTCAACAGGACCCTCCACGTCAGCATGTTCCAGGT
                                              ttgtcagctctccatcctccttctcagctgctctgttctcgacagcttcgggggaact 65
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nilarity 57.7%;
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US-752861.
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Matches 45
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New pure mammalian osteogenic proteins - induce cartilage and endochondral bone formation when in association with a matrix Claim 26; Columns 143-148; 128pp; English.

The osteogenic protein when in association with a matrix can induce at the locus of an implant the full development cascade of endochondral bone formation including vascularisation, mineralisation and bone marrow differentiation. The osteogenic protein can also be used to repair both bone and cartilage in the treatment of osteoarthritis. This sequence encodes the pre-proform of the protein.

Sequence 1723 BP; 265 A; 624 C; 577 G; 257 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-1990;
18-OCT-1990;
04-DEC-1990;
04-DEC-1990;
04-DEC-1991;
22-FEB-1991;
20-DEC-1991;
28-JAN-1992;
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30-NOV-1993.
08-APR-1988;
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Q53155;
Q6-JUN-1994
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07-SEP-1990;
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Osteogenic protein; bone; cartilage; matrix; osteoarthrit.
repair; vascularisation; mineralisation; differentiation;
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                                               gattccgcagccttccaa
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US-483913.
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-69.052 Million cell updates/sec
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Copyright (c) 1993 - 2000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Primates; Cat
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IRARGAAGYGINSRKFEFETSPDSF5ISGESSQVVMIAISAAVAIILLTVVIYVLIGR
FCGYKSKHGADEKKLHFGNGHLKLPGLRTYVDDHTYEDDTQAVHEFAKELDATVISH
KVVGAGEFGEVCSGRLKLPSKKEISVAIKTLKVGYTEKQRADFLGEASIMKGQFDHPII
IRLEGVVTKSKFVMIVTEYMENGSLDSFLRKHBAQFTVJQLLGHLRGIASGMKYLSDM
GYVHRDLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYTTRGGKIFIRWTSPEAIAY
RKFTSASDVWSYGIVLMEVMSYGERPYWEMSNQDVIRAVDEGYRLPPPMDCPAALYQL
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/db_xref="taxon:9606"
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FYKALDGNMKCAKCPPHSSTQEDGSMNCCEUNYFRADKDEVSMATRPSSPRAVI
NIBETSVILDWSWPLDTGGRKDVTFNIICKGGWNIKQCEPGSBNVRELPRQFGLTNT
TYTYTDLLAHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPVLTIKKDRTSR
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ISYESHGWEELSGVDEHYTPINLYWESDDDHGYKEREHQPTKIDTIAADESETQMDLGKFT
LRDCNSIPLYLGTCKETFINLYWESDDDHGYKEREHQPTKIDTIAADESETQMDLGKFT
ILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPM
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TTGDWLNGVETAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKAL
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/db_xref="GI:1247487"
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Catarrhini; Hominidae; Homo.
1 to 3132)
                                                                          GI:2830140
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                                                                                                                                                                                                                                                                                                                                                                   Score 87; DB 5; I
Pred. No. 2.6e-18;
; Mismatches 0;
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Best Local :
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Boyd, A.W., Simpson, R. John, Wicks, I., Ward, L. David and Wilkin
Method of screening for ligands to a receptor-type tyrosine
Patent: US 5674691-A 9 07-OCT-1997;
Location/Qualifiers
1. .3132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3149)
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Homo sapiens lymphoid tumor cDNA to mRNA.
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DSQSLVEVRGSCVNNSKEEDPRMYCSTEGERLVPICKCSCNAGYEERGFMCQACRPG
FYKALDGNMKCAKCPPHSSTQEDGSMNCRCENNYFRAKDEPSMACTRPSSGRRNYI
S NINETSVILDMSWPLDTGGRKDVFHNIICKKCGWNIKQCEPCSPNVRTLPROPGLTNT
TVTVTDLLAHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPVLTIKKDRTSR
NSISLSWQEEPHPNGIILDVSKYYEKQEQETSYTILRARGTNVTISSLKPDTYVFQ
IRARTAAGYGTNSRKFEFETSPDSFSISGETSVATLAISAAVAIILLTVVIYVIGR
FCGYKKKHGADEKKLHEGNGHLKLPGLRTYVDDYTAAVBFTAKELDATNISID
KVVGAGEFGEVCSGRLKLPSKKEISVAIKTLKVGYTEKQRRDFLGEASIMGQFDHPNI
IRLEGYVTKSKFVMIYTEYMENGSLDSFLKKHDAQFTVIQLVGMLRGIASGMKYLSDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
709 c 761 g
                                                               GYVHRDLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYTTRGGKIPIRWTSPEAIAY
                                                                                                                                                                                                                                                                                                                                             /product="receptor protein kinase"
/protein_id="AAA58633.1"
/db_xref="Gi:183932"
/translation="MDCQLSILLLLSCSVLDSEGELIPOPSNEVNLLDSKTIQGELGW
TTGDWLNGVRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKAI
                                                                                                                                                                                                                                                                                                       ISYPSHGWEEISGYDEHYTPIRTYQYCNYMDHSQNNWLRTNWYPRNSAQKIYYELKFT
LRDCNSIPLYLGTCKETFNLYYMESDDDHGYKFREHQFTKIDTIAADESFTQMDLGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HEK"
101. .3052
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/db_xref="taxon:9606"
/cell_line="LK63"
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!01. .3052
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Pred. No. 2.6e-18;
; Mismatches 0;
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                                                          Query Match
Best Local Similarity
Matches 71; Conserv
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gaactgattccgcagccttccaatgaa 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 2032)
Sajjadi, F.G., Pasquale, E.B. and Subramani, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA
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37; Conservative
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LKLNTEIREVGPVNKKGFYLAFODVGACVAL/SVRVYFKKCPFTVKNLAMFPDTVPMD
SQSLVEVRGSCVNNSKEEDPFNYCSTGEGEMLVPIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPHISSTQEDGSMACRCENNYFRAEKDPSMACARPSAPRNVIS
INETSVILDWSWPLDTGGRKDITFNIICKKCGWNVRQCEPCSPNVRFLPRQLGLTNTT
VTVTDLLAHTNYTFEIDAVNGVSELSSPPRQXAAVSITTNQAAPSPVMTIKKDRTSRN
                                                                                                                                                                        RARTAAGYGTNSRKFEFETSPDCMYYFSF"
2010. .2015
                                                                                                                                                                                                       SISLSWQEPEHPNGIILDYEVKYYQKQEQETSYTILRARGTNYTISSLKPDTTYVFQI
                                                                                                                                                                                                                                                                                                      /translation="MDCHLSILVLLGCCVLSCSGELSPQPSNEVNLLDSKTIQGELGW
ISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFT
                                                                                                                                                                                                                                                                                                                                    /product="Mek4 secreted"
/protein_id="AAA39522.1"
/db_xref="GI:454829"
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Mus musculus"
/strain-"IRC x Swiss Webster"
/db_xref-"taxon:10090"
/dev_stage-"11.5 day embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , 1994 this sequence version replaced gi:199121 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                           'tissue_type="embryo"
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                                                      Score 61.4; DI
Pred. No. 5.2e<sup>o</sup>
0; Mismatches
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Pred. No.
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hes 0;
                                                         DB 12;
.2e-10;
les 16;
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                                                                                       2032;
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Matches

Similarity

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Rattus no
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II-1 beta alters the expression of the receptor tyrosine kinase gene r-EphA3 in neonatal rat cardiomyocytes
Am. J. Physiol. 274 (1), H331-H341 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 3077)
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Rattus norvegicus
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Y.Y., McTiernan, C.F. and Feldman, A.M.
                                                                                                                                         877
                                                                                                                                                                                                                                      /product="cph-related receptor tyrosine kinase homolog"
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ILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVVVVFKKCPFTVKNLAMFPDTVPM
DSGSLVEVRGSCVNNSKEEDDPFMYCSTEGEWLVPIGKCTCNAGYEERGFICACRPG
FYKALDGVAKCTKCPPHSSTQEDGSMNCRCENNYFRAEKDPPSMACTRPPSAPRNVIS
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INTVTVLLAHTNYTFEIDAINGVSELSSPPRQFFAAVSITINQAAPSPVMTIKKDRTSR
NSISLSWQEPEHPNGIILDYEWKYYEKQEQETSYTILAARGTNVTISSLKPDTTYVFQ
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FCGYHKSKHSSDEKRLHFGNGHLRLPGLFRTYDDPTQAVHEFAKELDATNIAI
DKVVGAGEFGEWCGSTLKLPSKKEISVAIKTLKVGYTEKQRRDFLGEASIMGQDTHPN
IIRLEGVYTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGMKYLSD
MGYVHRDLAAANILINSNLVCKVSDFGLSRVLEDDDEAAYTTRAGKKIFVRWTSPEATA
VERTTERS SCNUGSCGTULWFWKGGEBDFWARTENDFLAGKIFFRWTSBEATA
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                              HTTGDWLNGMRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKA
                                                                                                                                                                                                                          YRKFTSASDVWSYGIVLWEVMSYGERPYWEMSNQDVIKAVDEGYRLPLPMDCPAALYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="neonatal"
/cell_type="cardiomyocytes"
1. .3077
                                                                                                                                                                                                        LMLDCWQKDRNNRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLDQSNVDIATF
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                         70.6%;
Score 61.4; DB 12;
Pred. No. 5.4e-10;
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                                             ATGGATTGTCACCTCCATCCTCGTCCTGCTCGGCTGCTGCGTCCTCAGCTGCTCCGGA 148
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Sajjadi,F.G., Pasquale,E.B. and Subramani,S. Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUSMEK4 3197 bp mRNA ROD 15-FEB-1994 MUSMEK4 3197 bp mRNA ROD 15-FEB-1994
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Mus musculus (strain IRC x Swiss Webster) 11.5 day embryo embryo
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TRLEGYVTKSKPEMIVTEYMENGSLDSFLRKHDAGFTVQDVGALRGIASGMKYLSDM
GYVHRDLAANNILINSMLVCKVSDFGLSRVLEDDPEAAYTTRGGKIPIRMTSPEAMSY
RKFTSASDVMSYGIVLMEVMSYGERPYSQMSNQDVIKAVDERYRLPPPMDCPAALYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYTTDLLAHTINYTFEIDAVNGVSELSSPPRQYAAVSĪTTNQAAPSPVMTIKKDRTSRN
SISLSMQEPEHPNGIILDYEVKYQKQDQETSYTILRAAGTNUYTSSLKEDTTYVEQI
RARTAAGYGTUSKKFEBEETSPDSFSISGENSHYVMIAISAAVAIIVLTYVTYULVGRE
CGYHKSKHSAEEKRLHEGNGHLKLPGLRTYVDPHTYEDPTQAVHEFAKELDATNISID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPPHSSTQEDGSMNCRCENNYFRAEKDPPSMACARPPSAPRNVISN
INETSVILDWSWPLDTGGRKDITFNIICKKCGWNVRQCEPCSPNVRFLPRQLGLTNTT
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/strain="IRC x Swiss Webster"
/db_xref="taxon:1090"
/dev_stage="11.5 day embryo"
/tlssue_type="embryo"
Rajaran
                                                                                                                                                                                                                                                                                                         MLDCWQKDRNNRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLDQSNVDIATFH
TTGDWLNGMRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISTIKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MDCHLSIIVLLGCCVLSCSGELSPQPSNEVNLLDSKTIQGELGW
| ISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPNSAQKIYVELKFT
| LRDCNSIPLYGTCKETFNLYYMESDDHGVKFREHQETKIDTIAADESSTQMDLGSRI
| LKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="receptor tyrosine kinase"
/protein_id="AAA39521.1"
/db_xref="GI:199120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Mek4"
/codon_start=1
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                                                                                                                                                      70.6%;
                                                                                                                              Score 61.4; DB 12;
Pred. No. 5.5e-10;
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* NOTE: This record contains 87 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 53997)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 53997)
Waterston, R.H.
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AC021186.1 GI:6693396
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HOMO Sapiens clone RP11-744D14, LOW-PASS SEQUENCE SAMPLING.
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             2: gap of unknown length
2: contig of 850 bp in length
3: contig of 439 bp in length
1: contig of 439 bp in length
3: contig of 404 bp in length
5: contig of 404 bp in length
6: gap of unknown length
7: contig of 842 bp in length
7: gap of unknown length
7: gap of unknown length
8: contig of 446 bp in length
8: contig of 446 bp in length
8: contig of 470 bp in length
8: contig of 613 bp in length
6: contig of 133 bp in length
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location For further information about this sequence, visit our sequence analysis of the sequence o
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Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E.,
Blazej, R. G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,
Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, S. H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S.,
Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R.,
Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R.,
Presidenting of Drosophila chromosome 2R, region 55C1-55C4
Unpublished (1997)
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Celniker, S. George, B., Galle, B., Sylvashe, B. B., Unching, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B. B., Unching, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B. B., Unching, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B., B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B., B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B., B.,
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Celniker, S. E., George, B., Galle, B., Sylvashe, B., Sylvashe, B.,
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Celniker, S. E., George, B., Galle, B., Sylvashe, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B., Sylvashe, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B., Sylvashe, B., Sylvashe, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B., Sylvashe, B.,
Celniker, S. E., George, B., Galle, B., Sylvashe, B.,
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1 (bases 1 to 84551)
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AC003465 AC003466 AC003467 AC003468 AC003469 AC003470
AC004295.1 GI:3347818
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19310 c 19295 g 23321 t
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/db_xref-"taxon:7227"
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Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 agcc
Direct Submission

Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 26, 1999 this sequence version replaced gi:5763790.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC017563
Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                       HSRYR7CC1 119118 bp DNA PRI 12-DEC-1999
Human DNA sequence from clone XX-PRYR7CC1 on chromosome 22 Contains an STS, GSSs, genomic marker D22S928, tc and ca repeat polymorphisms and a putative CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was identified as CDM:10211270 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (10-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
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Pred. No. 31;
0; Mismatches 22;
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, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 120625;
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This sequence was generated from part of bacterial clone contigs of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This sequence is not the entire insert of clone X-PRXR7CC1 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The true left end of clone XX-PRYR7CC1 is at 1 in this sequence. The true left end of clone CTA-217C2 is at 119019 in this sequen The true right end of clone RP4-753M9 is at 50597 in this sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
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                                                                                                                                  6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
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                                                                                                                                                                        6178. .6472
/note="AluSq repeat: matches 1.
6473. .6500
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/note="12_copies 6 mer cccccg
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77. .504
                                                                                                                                                                                                                              note="MER94 repeat: matches 47.
                                                                                                                                                                                                                                                                   'note="MIR repeat: matches 70. .172 of consensus"
                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 95.
i999. .6097
                                                                                                                                                                                                                                                                                                                                                                         /note="AluSg repeat: matches 1. .307 of
1418. .4542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="Single clone region"
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                                                                  'note="MER21B repeat: matches 706. .789 of consensus"
                                                                                                                                                 note="MER94 repeat: matches 27.
                                                                                                                                                                                                                                                                                                                                              'note="AluJo/FRAM repeat: matches 152. .276 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Single clone region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4. .2817
|te="37 copies 2 mer cc 66 conserved"
| 8. .3707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="15 copies 26 mer 56 conserved" .488
                                                                                                                                                                                                                                                                                                                                                                                                             "15 copies 2 mer tt 90 conserved" 4249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copies 40 mer 76 conserved"
                               repeat: matches 18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 conserved"
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                               . 132
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                                                                                                                                               .47 of consensus"
                                                                                                                                                                                                                            .107 of consensus
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                                                          /note="MLT1-INTERNAL r.
consensus"
19869. 201/0
                      /note="AluJo repeat: matches 18. 20218. .20385
                                                                                                                                                                                                                                                                                                                         /note="AluSq repeat: matches 1.
complement(15768. .16376)
/note="match: GSS: Em:AQ476535"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10871. .11171
/note="AluJo repeat: matches 1.
11190. .11487
/note="AluSx repeat: matches 1.
11610. .11726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSq repeat: matches 57. .311 of consensus"
10736. .10821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 13. .300 of consensus"
9266. .9580
/note="AluSp repeat: matches 5. .313 of consensus"
                                                                                                                                           consensus
                                                                                                                                                                                                                                                                                                                                                                                      /note="26 copies 2 mer aa 73 conserved"
17222. .17308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="143 copies 2 mer gg 59 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3105. .8229
/note="Alusq/x repeat: matches 9.
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note="MER2 repeat: matches 269. .343 of consensus"
note="MLT1B repeat: matches 1.
                                                                                                                                                                'note="MLT1-INTERNAL
                                                                                                                                                                                                     'note="AluSx repeat:
                                                                                                                                                                                                                                        note="AluY repeat: matches 1. .310 of consensus"

18508. .18616

"Once="LIPA6 repeat: matches 6035. .6143 of consensus"
                                                                                                                                                                                                                                                                                                                     note="18 copies 2
                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="MIR repeat: matches 73. .226 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Alusp_repeat: matches 1. .312 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="L1MA10 repeat: matches 6135. .6322 of consensus" L0481. .10735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MIR repeat: matches 34. .240 of consensus"
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note="AluJo/FRAM repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26. .15335
te="LlP3 re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24. .14886
_e="LIPA10 repeat: matches 5476. .6165 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 6. .368 of consensus"
                                                                                                                                                                                                                                                                                                                       mer tg 91 conserved"
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    .180 of consensus"
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Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Feb 2, 2000 this sequence version replaced gi:6693437.
                                                                                                                                                                                                           2 (bases 1 to 183776) Waterston, R.H.
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 183776)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AC017104 183776 bp DNA HTG 02-F) HOMO Sapiens clone RP11-56215, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                     AC017104.3 GI:6855250
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      AC017104
AC017104.3
                                                                                                                                                                                                                                                                                                                                                                                                                       pieces
                                                                                                                                                                                                                                                        The sequence of Homo sapiens clone
                                                                                                                        63108, \ \mbox{USA} Feb 2, 2000 this sequence version replaced g1:6693437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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/notes Alusp repeat: matches 1. .303 of consensus 70685. .20736
/notes MLTIB repeat: matches 180. .234 of consensus 70737. .21016
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complement(24215..24582)
/note="match: GSS: Em:AQ375812"
24487...24919
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/note="match: GSS: Em:AQ529159"

/note="match: GSS: Em:AQ569063"

/note="match: GSS: Em:AQ569063"
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22386. .22
/note="15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSg repeat: matches 1.
21017. .21215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MLTID repeat: matches 6. .94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.98;
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22415
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Pred. No. 35;
0; Mismatches
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                                                                            Genome Sequencing Center
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                               FEATURES
                source
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Chemistry: Dye-primer ET; 88% of reads
Chemistry: Dye-terminator Big Dye; 12% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 168893 bases at least Q40
Consensus quality: 174250 bases at least Q30
Consensus quality: 177018 bases at least Q20
Insert size: 183700; agarose-fp
Insert size: 183776; sum-of-contigs
Quality coverage: 3.77 in Q20 bases; agarose-fp
Quality coverage: 3.55 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; 88% Sequencing vector: plasmid;
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of tw.

p of unknown length
gap of unknown length
gap of unknown length
contig of 8335 bp in length
gap of unknown length
y: contig of 9420 bp in length
gap of unknown length
gap of unknown length
slove contig of 9433 bp in length
gap of unknown length
127447: contig of 14347 bp in length
gap of unknown length
141478: contig of 14317 bp in length
gap of unknown length
183776: contig of 25149 bp in lr
Location/Qualifiers
1. 183776
/organism="Homo sapiens"
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gap of unknown 1
3630: contig of 2411 b
gap of unknown 1
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-Nov-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 29, 1999 this sequence version replaced gi:6468554.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature key
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                                                                                                                                                                                                                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RP1-72EL7 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pleter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[] (bases 1 to 90299)
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                                                                                                                                                                     sequence is the entire insert of clone RP1-72E17
Location/Qualifiers
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/ 44968 c 44823 g 47139 t
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/chromosome="6"
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7992. .8401
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clone RP1-72E17 on chromosome
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                                                                                                                                Homo sapiens chromosome 19 clone CITB-H1_2329C7, SEQUENCE, 44 unordered pieces.
Eukaryota; Metazoa; Chordata; C
Eutheria; Primates; Catarrhini;
1 (bases 1 to 187701)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                            Homo sapiens
                                                                                                    AC010485.2 GI:6693194
HTG; HTGS_PHASE1; HTGS_DRAFT
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complement(54830. .55149)
/note="match: GSS: Em:AQ039170"
55156. .55504
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8184. .8478
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11636. .11917
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/note="match: GSS:
1 20192 c 20337 g
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/note="match: STS:
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                                            Catarrhini;
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                                             Hominidae;
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                                                           Vertebrata; Mammalia;
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Center Code: JGI
Web Site: http://www.jgi.doe.gov
-----Summary Statistics
Consensus quality: 12926 bases at least Q40
Consensus quality: 142143 bases at least Q30
Consensus quality: 147093 bases at least Q20
Estimated insert size: 187701; sum-of-contigs estimation
Estimated insert size: 125880; sagarose-fp estimation
Quality coverage: 8.86x in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.95x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jan 14, 2000 this sequence version replaced g1:5882452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1 to 187701)
DOE Joint Genome Institute.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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RESULT 14 ALL38881 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Qy 68 to 1 Db 181214 Tv	Qy 8 g. Db 181274 G.	Query Match Best Local Matches 4	BASE COUNT ORIGIN	source	FEATURES																				
AL138881 211385 bp Homo sapiens chromosy PROGRESS ***, 50 uno: AL138881 GI:69828: HTG; HTGS_PHASE1.	ttccgcagccttc 80 reccgcaggaTTC 181202	tcagctctccatcctcc ACAGCTTCCCCTCTCCCTCC	ch 32.4% 1 Similarity 61.6% 45; Conservative	/Chromesme="19" / Chrome="CITB-H1_2 / Chome="CITB-H1_2 47607 a 47529 c 45578	1187701 /organism=	 124846 187701: contig Location/Qualifier 	* 102398 124845	83414 102397	69869 83413	60770 69868	59473 60769	* 56459 59472	54516 56458	52830 54515	50802 52829	48949 50801	47444 48948	45614 47443	44463 45613	43165 44462	* 41919 43164	39807 41918	* 38429 39806	* 36810 38428	* 35295 36809	* * 34099 35294:
DNA DNA clone RP11-9 rdered pieces.		gtcagctctccatcctccttctcagctgctctgttctcgacagcttcggggaactga 	; Score 28.2; DB 4; Pred. No. 50; O; Mismatches 2	929	"Homo sapiens"	of 62856 s	contig	contig of 18984	contig of 1354		of 1297	of 3014	of 1943	of 1686	contig of 2028		of 1505	of 1830	of 1151	of 1298	of 1246	tig of 2112	of 1378	of 1619	contig of 1515	gap of unknown contig of 1196
HTG 05-FEB-2000 528H16, *** SEQUENCING IN		gacagcttcggggaactga 67 ACTAGATTCGGGGCCATTT 1812	4; Length 187701; 8; Indels 0; Gaps	320 others		in length.	in length ath	in length	in length	gth in length	gth in length	in length	gth in length	in length	in length	gth in length	gth in length	gth in length	in length	in length	in length	in length	in length	in length	in length	yth In length

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2 (bases 1 to 307834)
DOE Joint Genome Institute.
Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 307834)
DOE Joint Genome Institute.
                                                                                                                 Unpublished
                                                                                                                                      Sequencing of Human Chromosome
                                                                                                                                                                                                                                                       Homo sapiens
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-----Summary Statistics
Consensus quality: 224141 bases at least Q40
Consensus quality: 249816 bases at least Q30
Consensus quality: 258890 bases at least Q20
Estimated insert size: 307834; sum-of-contigs estimation
Estimated insert size: 120000; pulse field gel estimation
Quality coverage: 15.47x in Q20 bases; pulse field gel estimation
Quality coverage: 6.03x in Q20 bases; sum-of-contigs estimation
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Center Code: JGI
Web site
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BASE COUNT ORIGIN

Query Match Best Local S Matches 48 FEATURES

source

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

REFERENCE

KEYWORDS SOURCE ORGANISM

ACCESSION VERSION RESULT 15 AC010475/c LOCUS

DEFINITION

8 8 8 8

205236

67

205176

ORIGIN

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Query Match
32.4%; Score 28.2; DB 44; Length 307834;
Best Local Similarity 61.6%; Pred. No. 52;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps
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0

MATCHES 45; CONSERVATIVE 0; MISMATCHES 28; INDELS 0; Gaps

Oy 8 gtcagctctccatcctccttctcagctgctctgttctcgacagcttcggggaactga 67

Ob 297411 GACAGCTTCCCCTCCCTCCTCCAGCCTGCTTCCAGATTCCAGATTCGGGGCCATTT 297352

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Db 297351 TGCCGCAGGATTC 297339

68 ttccgcagccttc

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Search completed: May 15, 2000, 11:43:02 Job time: 18609 sec

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196.854 Million cell updates/sec
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Minimum Maximum

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammali;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
1 (bases 1 to 435)
1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
  The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                H38363 435 bp mRNA EST 16-AUG-1995
PP50904.rl Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:190902 5', similar to 9b:M83941 TYROSINE-PROTEIN KINASE
RECEPTOR HEK PRECURSOR (HUMAN);, mRNA sequence.
H38363
H38363.1 GI:907862
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AQ473555
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AA103674
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                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                            Vertebrata; Mammalia;
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AA103674 mc40c10.r
AA466804 vd90g11.r
AA466804 vd90g11.r
AA000659 mg26a04.r
AA76271 vv60g01.r
AA123801 mp96d07.r
AA123801 mp96d07.r
AA123801 mp96d07.r
AA233555 HS_5060_A
AQ6433555 HS_5060_A
AQ6433555 HS_50610.x
AQ761950 xq29c10.x
A165562 tt13907.x
A16556283 wb30e10.x
A165565522 tt13907.x
A16556561 KP5200 A
AQ641860 RPCI-11-3
AQ541860 RPCI-11-3
AQ541860 RPCI-11-3
AQ54255 HS_500A
AQ656077 Sheared D
H17411 ym44c11.s1
AA720125 33318 Lem
AQ861085 nbeb0016E
AI195110 u160906.x
AA720125 33318 Lem
AQ861085 nbeb0016E
AI195110 u160906.x
AA720125 33318 Lem
AQ861085 nbeb0016E
AI195110 u160906.x
H55902 yr02c08.s1
AA038832 m195912.r
AA038832 m195915.r
AA0365614 Sheared D
AQ708302 HS_5569_A
N38130 19357 Lambd
AQ708302 HS_5569_A
N38130 19357 Lambd
AQ77466 AU077466
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AA212205 mu80b06.r
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AA726779 vu42f03.r
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AA586761 nn71c10.
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                                                             Marra, M.
                      REFERENCE
AUTHORS
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Eukaryota; Metazoa; Catarrhini; Hominico, Eutheria; Primates; Catarrhini; Hominico, 1 (bases 1 to 306)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Insert Size: 2663
High quality sequence stops: 276
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2663
Std Error: 0.00
Seq primer: M13Rev
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                       mRNA sequence.
AA586761
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nn71c10.sl NCI_CGAP_Lar1
                                                                                                                                                 Homo sapiens
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ilarity 100.0%;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:3847311"
/db_xref="taxon:9606"
/clone="IMAGE:190902"
/clone_lib="Soares retina N
/sex="male"
/tissue_type="retina"
/dev_stage="55_year_old"
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                                                                                                                                                                                                       GI:2397575
                                                                                                             Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66; DB 23;
Pred. No. 4.1e-14;
); Mismatches 0;
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                                                       Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 435
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Best Local
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Fax: 314 485 1014
Email: est@watson.wustl.edu
Insert Size: 2443
Insert Size: 2443
High qality sequence stops: 337 Source: IMAGE Consortium, LLNL This
Clone is available royalty-free through LLNL; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
                                                                                                                                               Unpublished (1995)
Unpublished (1995)
On May 9, 1995 this sequence version replaced
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Nov 29, 1993 this Contact: Robert Stra Tel: (301) 496-1550
                                                                                                                                                                                                                                                                            Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)
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IMAGE:36023
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                                                                                                                                                                                                                                                                   Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
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314 286 1810
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t: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert_Strausberg@nih.gov
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Soares infant brain lNIB
3 3', mRNA sequence.
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N87424/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 bp
Loos Human fetal hear
clone L3865 5' simi'
mRNA sequer
                                                                                                                                                                                                                                                                                         Department of Laboratory Medicine and University of Toronto
Banting Institute, 100 College St., To
                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
On May 9, 1995 this sequence version replaced gi:802248.
Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: Promega -21ml3 High quality sequence stop
                                                                                                                                                                                                                                          Email: liewcc@utcc.utoronto.ca
                                                                                                                                                                                                                                                                           Tel: 4169788758
                                                                                                                                                                                                                                                                                                                                                                                               cDNAs from fetal heart (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                  Liew, C.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XLI-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). CDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."
                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="L3865"
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                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GDB:408524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 etal heart, Lambda ZAP Express Homo sapiens cDNA similar to RECEPTOR PROTEIN-TYROSINE KINASE (HEKI1),
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Pred. No. 5.8;
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 835)

Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A., Hirata, M., Suzuki, Y., Sasaki, M. and Sugano, S.

Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method Unpublished (199)

On May 18, 1998 this sequence version replaced gi:3137227.
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AU080921 Sugano mo
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                       Similarity
                                                                                                                                                 202
                                                                                                                                                                                                                                                                                                                                                                                          l: khashi@nih.go.jp
http://www.nih.go.jp/yoken/genbank/.
Location/Qualifiers
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Sugano mouse
                                                                                                                                                                                                                                                                                                                                   /strain="C57BL"
/db_xref="taxon:10090"
/clone="MNCb-6241"
                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                             /sex="female"
                                                                                                                                                                                                                                                                                                                       /clone_lib="Sugano mouse brain mncb"
                                                                                                                                                                                                                                                                                                                                                                    'organism="Mus musculus"
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Pred. No. 14;
0; Mismatches
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Pred. No. 11
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clone MNCb-6241
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                                                      EST.
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                                       house mouse.
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8 tactggattcaaaaacaattcaaggggagctgggctggatctcttatccatcacatggg 66
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Eukaryota; Metazoa; C
Eutheria; Rodentia; S
1 (bases 1 to 254)
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Unpublished (1999)
On Mar 10, 1998 thi
Contact: Chie Owa
                                                                                                                                                                                                     mq73c06.rl Stratagene mouse melanoma (#937312) Mus
clone IMAGE:584362 5', mRNA sequence.
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AV080438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostabilization and thermoactivation of thermolabile enzymes k trehalose and its application for the synthesis of full length cDN (Proc. Natl. Acad. Sci. U.S.A. 95(2):524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

polymerase visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV080438.1 GI:5211886
EST.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 341)
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AA125015.1 GI:1684192
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Tel: 81-298-36-9145
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/clone="2210414F24"
/clone_lib="Mus musculus stomach C57BL/6J adult"
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/strain="C57BL/6J"
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62 c 58 g
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/tissue_type="stomach"
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Fukunishi,Y., Funayama,T.,
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                                                                                                                AUTHORS
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On Sep 12, 1996 this sequence version replaced Contact: Marra M/MOUSE EST Project
WashU-HHM Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis,
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentla; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 364)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Location/Qualifiers
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Fax: 314 286 1810
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/tlssue_type="melanoma"
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/clone="IMAGE:584362"
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On May 18, 1995 this sequence version rep.
Contact: Marra M/Mouse EST Project
Washin-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seatt
Tel: (206) 616-3618
Fax: (206) 616-3887
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AQ338519.1
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HS_3118_B1_C10_MR CIT Approved Human Genomic Sperm
                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:397675
                                                                                                                                                                                                                   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 314 286 1810
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/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. From M2 cells, a highly metastatic derivative of
the K-1735 (mouse) melanoma. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTTTT 3'"
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/clone_lib="Stratagene mouse melanoma (#937312)"
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AUTHORS
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                                                                                                                                                                                                                                                                   Unpublished (1996)
On Apr 14, 1993 this sequence version repl.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          w30350 416 bp mRNA EST 11-SEP-1996 mc25e10.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:349578 5' similar to PIR:S33561 S33561 ref(2)P protein fruit fly; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 416)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3118 row: F column: 19
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Location/Qualifiers
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                                                                                                                       primer: ETPrimer
                                                                           quality sequence stop: 414.
Location/Qualifiers
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314 286 1810
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E-Col1 DH10B"
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:349578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="Plate=3118 Col=19 Row=F"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 19;
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AA726779/c
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Matches 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
On May 5, 1995 this sequence version repla
Contact: Marra Myhouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA726779 426 bp mRNA CATTER OF THE LCK SH2 DOMAIN B-CELL ISOFORM ;,
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1 (bases 1 to 426)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
AA726779
AA726779.1 GI:2744486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA726779
                                                                                                                                     MGI:641173
                                                                                                                                                              Email: mouseest@watson.wustl.edu
This_clone is available royalty-free through LLNL;
                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                            Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 63.9
39; Conservative
                                                                                                                                                IMAGE Consortium (info@image.llnl.gov) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                        primer: -28m13 rev2 ET from Amersham
h quality sequence stop: 419.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:1194077"
/clone_lib="Barstead mouse myotubes MPLRB5"
                                                /strain="C3H"
                                                            /organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.1%;
63.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25.8; DI
Pred. No. 19;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA103674 434 by mRNA EST 29-OCT-1996 modOc10.r1 Life Tech mouse embryo 15 5dpc 10667012 Mus musculus cDNA clone IMAGE:556050 5' similar to TR:G1184951 G1184951 PHOSPHOTYROSINE INDEPENDENT LIGAND P62B FOR THE LCK SH2 DOMAIN B-CELL ISOFORM; mRNA sequence.
                                                                                                                                                                                                                                                                                  Unpublished (1996)
On Nov 29, 1993 this sequence version replaced Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 434)
                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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AA103674.1 GI:1649894
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/organism="Mus musculus"
/strain="0.57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:556050"
/clone_lib="Life Tech mou:
/tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="C2C12"
/lab_host="DH10B"
                                                                                                                              Location/Qualifiers
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Pred. No. 19;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project Unpublished (1996)
On Jan 25, 1995 this sequence version repl Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Lc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA466804 438 bp mRNA EST 11-JUN-1997 vd90911.r1 Soares mouse NbMH Mus musculus CDNA clone IMAGE:8077908 5' similar to TR:G1184951 G1184951 PHOSPHOTYROSINE INDEPENDENT LIGAND P62B FOR THE LCK SH2 DOMAIN B-CELL ISOFORM ;, mRNA sequence
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                                                                                                                                                                                                                                                              vector to vector length is 511
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 409.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                            Putative full length read
                                                                                                                                                                                                                                                                                                                                                              MGI:484252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA466804.1
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108 c 120 g 105 t
/db_xref="taxon:10090"
/clone="IMAGE:807908"
                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="15.5dpc embryos"
/lab_host="DH10B"
                                                                                                                                    /sex="male"
                                                                                                                                                      /clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 to 438)
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63.9%;
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Sciurognathi; Muridae; Murinae; Mus.
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Mismatches
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RESULT 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
On Apr 14, 1993 this sequence version replaced g1:693679.
Contact: Marra MyMouse EST project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Marra M., Hillier L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mg26a04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:424878 5' similar to PIR:S33561 S33561 ref(2)P protein filt fly; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                  MGI:259430
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                                                                                                                                                                                                                                                                                    quality sequence stop: 344.
Location/Qualifiers
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      3']; double-stranded cDNA was ligated to Eco RI adapt (Pharmacia), digested with Not I and cloned into the I and Eco RI sites of the modified pm713 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatir
                                                                                                                                                                                      /organism-"Mus musculus"
/strain-"C57BL/6J"
/db_xref-"taxon:10090"
/clone-"IMAGE:424878"
                                                                                                                                                    /sex="unknown"
                                                                                                                                                                      /clone_lib="Soares mouse
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on equal amounts of mRNA
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Pred. No. 1
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ACCESSION
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AA762271/c
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JOURNAL
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Best Local
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1 (bases 1 to 505)

1 (bases 1 to 505)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Geisel,S., Kucaba,T., Lacy,M., Tan,F., Underwood,K., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 8, 1995 this sequence version replaced gi:801194.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vw60g01.rl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1248240 5' similar to TR:Q13502 Q13502 PHOSPHOTYROSINE INDEPENDENT LIGAND P62B FOR THE LCK SH2 DOMAIN B-CELL ISOFORM ;,
                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                       IMAGE Consortium (info@image.llnl.gov)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
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133 c 140 g 94 t 1 others
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then priwith a Not I - oligo(dT) primer. Double-stranded cDNI ligated to Eco RI adaptors (Pharmacia), digested with
                                                                                                           /organism="Mus musculus"
/db_xref="taxon:1090"
/clone="IMAGE:1248240"
/clone_11b="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Pred. No. 19;
0; Mismatches
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Mus.
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cDNA was
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I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library is normalized. Library base COUNT 120 a 132 c 122 g 131 t

Query Match 39.1%; Score 25.8; DB 38; Length 505;

Best Local Similarity 63.9%; Pred. No. 19;

Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 6 tctactggattcaanaacaattcaaggggagctggatctttatccatcacatgg 65

Db 132 TCTACGTGATGCAACTACAAGACAAAGGGGGTGGGGCTTGGCCACAGCACTATCACAATG 73

Qy 66 g 66
Db 72 G 72

Search completed: May 15, 2000, 11:20:19

Search completed: May 15, 2000, 11:20:19
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OM nucleic

Sequence

14, Appl 14, Appl 14, Appl 22, Appl 22, Appl 20, Appl 19, Appl 19, Appl 17, Appl 17,

Sequence Sequence Sequence Sequence

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Title:
Perfect score:
Sequence:
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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
6: /cgn2_6/ptodata/
7: /cgn2_6/ptodata/
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length: 1000000
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Match
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     US-09-104-340-7
66
1 gtcaatctactgga
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Gapop 10.0 , Gapext 1.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/6COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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45 summaries
 US-08-167-919A-9
US-08-715-106-9
US-08-715-106-9
US-08-449-645A-12
US-08-702-367A-12
PCT-US95-046B1-12
US-08-49-537A-102
US-08-49-537A-102
US-08-49-645A-10
US-08-60-0419-1
US-08-60-0419-1
US-08-60-60419-1
US-08-60-60419-1
US-08-60-60419-1
US-08-60-60419-1
US-08-616-34
PCT-US95-046B1-10
US-08-616-34
PCT-US95-046B1-14
US-08-222-616-34
PCT-US95-046B1-14
US-08-222-616-34
PCT-US95-046B1-14
US-08-222-616-34
PCT-US95-046B1-14
US-08-222-616-34
PCT-US95-046B1-14
US-08-469-537A-100
PCT-US95-046B1-14
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Compugen
Sequence 9, Appli
Sequence 15, Appl
Sequence 15, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 102, Appl
Sequence 102, Appl
Sequence 1, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 10, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 10, Appl
Sequence 11, Appl
                                                                                                                                                                                                                                                                                                                                                  Description
                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,919A
FILING DATE: 18-APR-1994
CLASSIFICATION UNMBER: US/08/167,919A
FILING DATE: 11-JUN-1991
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-436
TELEFAX: (230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-167-919A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application Patent No. 5674691
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Boyd, Anuser J.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Ward, Larry D.
APPLICANT: Wikinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
TITLE OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: U.S.A.
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US-08-976-838-14
US-08-976-838-14
US-08-976-838-22
US-08-976-838-22
US-08-976-838-20
US-08-976-838-17
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Best Local S
Matches 66
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Patent No. 6020306
                                                                                                                                            FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 10-THN-1007
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9
                                                         FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
08/167,919
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247
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                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 18-API
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/01
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lin
                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Scully, Scott, Mur
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wicks, Ian
Ward, Larry D.
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100..3048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simpson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boyd, Andrew W.
                                              (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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                                                                                                                                                                                                                                                                                                                                       US/08/715,106
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Pred. No. 1.5e-16;
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US-08-715-106-9
                                                                               US-08-162-809-15
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Best Local S
Matches 66
                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15,
                                                                                                                                                                                 TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3254 base pairs
                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 514
ATTORNEY_AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-LJ
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 535-9001
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 CATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100 ues 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 catggg 66
                                                                                                           NAME/KEY:
                                                                                                                                         TOPOLOGY:
                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
   62; Conserv
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
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100..3048
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                 90.38;
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Score 59.6; DB 1;
Pred. No. 4.4e-14;
0; Mismatches 4
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                              Length 3254;
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Matches

Conservative

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Gaps

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US-08-702-367A-12
US-08-702-367A-12
; Sequence 12, Application US/08702367A
; Patent No. 5981246
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US-08-449-645A-12
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Best Local Similarity
Matches 46; Conserv
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                                                                        GENERAL INFORMATION: APPLICANT: Fox, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
                                         APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
             NUMBER OF SEQUENCES: 4
                                                                                                                                                                                            169 AATGGG 174
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                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/449,645A FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                      61 catggg 66
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TOPOLOGY: lin
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LOCATION: 1...
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   ADDRESSEE:
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nucleic acid
DEDNESS: single
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1840 Dehavilland Drive
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Amgen Patent Operations/RBW
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69.7%;
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Pred. No. 0.00031;
0; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3162 base pairs
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   STREET: 10% CITY: Thousand Oaks
STATE: California
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LENGTH: 3162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Lik
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                          ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
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CLASSIFICATION:
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ZIP: 91320
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1840 Dehavilland Drive
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69.7%;
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Pred. No. 0.00031;
0; Mismatches 20
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US-08-449-645A-16
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Best Local Similarity 69.7
Matches 46; Conservative
                                                            Matches
                                                                                        Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
                                                                                                                                                                               FEATURE:
                                                                                                                                                                                        TOPOLOGY: 11
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
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    288
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                       Local Similarity
                                                                                                                                                                                                                  LENGTH: 4529 base pairs TYPE: nucleic acid STRANDEDNESS: single
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LOCATION: 1...
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CTGCTGGATTCTAAAGCACAACAACAGAGTTGGAGTGGATTTCCTCTCCACCCAATGGG 347
                Thousand Oaks California
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1840 Dehavilland Drive
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Pred. No. 0.00031;
0; Mismatches 20;
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Pred. No. 0.0041;
0; Mismatches 1
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LOCATION:
US-08-702-367A-16
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INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Patent No.
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Best Local Similarity
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            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATEN: COMPATEN: COMPATEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: EPH-LIK
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                   TITLE OF INVENTION: EPH-Lik
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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CLASSIFICATION: 435
                                                                                                                                COUNTRY:
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STATE: California
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 APPLICATION NUMBER:
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1840 Dehavilland Drive
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186..3182
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PCT/US95/04681
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Pred. No. 0.0041;
0; Mismatches 18; Indels 0
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CLASSIFICATION:

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; LOCATION: 186
PCT-US95-04681-16
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                       INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 3906 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 42; Conserv
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                                                                                                                              APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler; Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEPAX: 914-345-7721
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
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APPLICATION NUMBER: US/08/469,537A
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LENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Diskette
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TITLE OF INVENTION: EHK AND ROR TYROSINE
TITLE OF INVENTION: KINASES
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
COFTWARE: FastSEQ Version 2.0
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road
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              unknown
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)N: 435
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Pred. No. 0.0041;
0; Mismatches 18;
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; FEATURE: CI; NAME/KEY: CI; LOCATION: 47; US-08-469-537A-102;
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                                                                                             Matches
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Best Local :
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                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHLA, TIMOTHY E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-8674
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                   TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb 1
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4.
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  722 AATGGG 727
                                                                                         y Match 44.2%;
Local Similarity 65.2%;
hes 43; Conservative
                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
61 catggg 66
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les 43; Conserv
                                                                                                                                                                                                                                      LENGTH: 4165 bases
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                                             1 gtcaatctactggattcaaaacaattcaaggggagctgggctggatctcttatccatca 60
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T: 460 Point San Bruno Blvd
South San Francisco
: California
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 Mismatches

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                                                                                         Score 29.2; DB 2; Length 4165;
Pred. No. 0.023;
0; Mismatches 23; Indels 0
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RESULT 12 US-08-440-815-1

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PCT-US96-00419-6
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Sequence 6, Application PC/TUS9600419
GENERAL INFORMATION:
APPLICANT: Thomas Clossek, Axel Ullrich, Birgit
APPLICANT: Millauer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (denentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
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TELECOMMUNICATION INFORMATION:
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NAME: Torchia, Timothy E
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/330128
FILING DATE: 27-0CT-1994
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CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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: USA
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415/952-9881
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                                                                                                                                                                                                                                                                                                                                       Score 29.2; DB 2;
Pred. No. 0.023;
0; Mismatches 23;
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MOLECULE TYPE:
PCT-US96-00419-6
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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2323
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Applicati
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Best Local :
                                COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00419
FILING DATE: January 3, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OFERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTMARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION MITTERS
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                 APPLICANT: Thomas Clossek, Axel Ullrich, Birgit
APPLICANT: Millauer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
   PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                            STREET: 633 West | CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
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STRANDEDNESS: sing
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January 3, 1995
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66.1%;
including application
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Pred. No. 0.14;
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PCT-US96-00419-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9600419 GENERAL INFORMATION:
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wazburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPA: (213) 955-0440
TELEX: 67-3510
                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                      INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomas Ciossek, Axel Ullrich, Birgit
APPLICANT: Millauer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                             SEQUENCE CHARACTERISTICS:
LENGTH: 4304
                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: Januar CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
ZIP: 90071
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Query Match 100.0%; Score 66; DB 1; Best Local Similarity 100.0%; Pred. No. 2.1e-16; Matches 66; Conservative 0; Mismatches 0;

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W09528484-A1.
26-OCT-1995; U04681.
14-APR-1995; US-229509.
15-APR-1994; US-229509.
(AMGE-) AMGEN INC.
FOX GM, Jing S, Welcher AA;
WPI; 95-373799/48.
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08-JUN-1995.
07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER R
Pasquale EB, Sajjadi FG;
WPI; 95-215266/28.
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Probes derived from the EPH-related PPKs Cek4 (Q90659) and Cek5 (Q90660) were used to isolate novel cDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues, as well as in the adult brain and retina. Sequence 3254 BP; 926 A; 737 C; 796 G; 795 T;
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Matches 46
                                                                               DNA encoding embryonic stem cell kinase, receptor tyrosine kinase - production of modulators and antibodies, useful to treat mucositis and other disorders involving epithelium claim 4; Page 48-54; 98pp; English.

Claim 4; Page 48-54; 98pp; English.

Chaim 4; Page 48-54; Page 48-54; 98pp; English.

Chaim 4; Page 48-54; Page 48-54; Page 48-54;

Chaim 4; Page 48-54;

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Chaim 4; Page 48-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
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20-DEC-1996; AU0826.
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                                                             as sense
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433. .3285
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                                                    produce recombinant Esk and antisense molecules
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9: Pred. No. 0.00
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receptor tyrosine kinase; mucositis;
rion; gene therapy; diagnosis; ss.
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0.00049;
                                                       polypeptides,
for diagnosis
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Matches 42
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Best Local S
Matches 43
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Claim 1; Page 66-72; 133pp; English.

CONAS (T02946-49) coding for 4 novel human EPH-like receptor protein tyrosine kinases; HEX5, HEX7, HEX8 and HEX11 (R85089-92), respectively, were isolated from a human foetal brain cDNA library using a directed PCR approach with primers (see T02960-61) based on conserved regions of receptor PTKs and EPH-like receptor PTKs. HEX5, HEX7 and HEX8 show extensive homology to the catalytic domain of chicken EPH-like receptors. Cek5, Cek7 and Cek8. HEX11 shows no homology to any known EPH-like receptor. The isolated cDNAs are used for prodn. of recombinant HEKS and chimeric receptors, in hybridisation assays, and
                  11-FEB-1999 (first entry)
Rat receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; E
neurotrophin activity; trkB; proto-oncogene; tyr
binding protein; BDNF; NT-3; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., use diagnostically and therapeutically to modulate receptor activations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPH-like receptor protein tyrosine kinase HEK11 cDNA EPH-like receptor protein tyrosine kinase; PTK; HEK1: human eph-like kinase; therapy; diagnosis; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC. Fox GM, Jing S, Welcher WPI; 95-373799/48.
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          Rattus sp
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42; Conserv
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US-229509.
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Pred. No. 0.00
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                                 tyrosine
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                                             Ehk -2;
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kinase rec
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Best Local S
Matches 43
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26-OCT-1995; U5-330128.
27-OCT-1995; US-486449.
07-JUN-1995; US-486449.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins
Claim 5; Fig 22; 194pp; English.
Claim 5; Fig 22; 194pp; English.
Claim 5; Fig 22; 194pp; English.
The present invention describes nucleic acid molecules for run-
The present invention described are the corresponding prot
run-2, ehk-1 and ehk-2. Also described are the corresponding prot
Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor
tyrosine kinases. The present sequence encodes rat Ehk-1.
tyrosine kinases. The present sequence encodes rat Ehk-1.
3906 BP; 1097 A; 876 C; 990 G; 943 T;
         AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in treatment and diagnosis of neuronal disorders and angiogenesis-related conditions.

Example 1: Page 47-49; 75pp: English.

A cDNA clone (T18893) codes for rat REK7 (R97853), an eph-related tyrosine kinase receptor, for which AL-1 (see also W97854) is a ligand. It was isolated using degenerate receptor tyrosine kinase primers (T18894-96) to amplify cDNAs of an adult mouse hippocampal cDNA library. A PCR fragment was used as a probe to isolate the full-length REK7 cDNA from a rat hippocampal cDNA library. An a rat hippocampal cDNA library. An constant of the constant contains the contains 
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01-DEC-1998.
06-JUN-1995;
17-MAR-1995;
                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC. Caras IW, Winslow JW; 96-239448/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REK7; eph-related tyrosine kinase receptor; AL-1; ligand; neurotrophic factor; neuropathy; angiogenesis; therapy; or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T18893 standard;
T18893;
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WPI; 99-044584/04.
P-PSDB; W83147.
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06-JUN-1995; US-469537.
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43; Conser
  fusion was used to screen
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541. .711
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712. .3324
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Pred. No. 0.03
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11-JUL-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES FC
(SUGE-) SUGEN INC.
Clossek T, Millauer B,
WPI; 96-333988/33.
                                                          Example 1; Page 115-116; 128pp; English.

EXAMPLE 1; Page 115-116; 128pp; English.

EDNA cloning using adult mouse brains and MDK1 T2 (T32962), that coded for truncated versions (W03423 and W03423, respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The CDNA clones can be used to produce MDK1 T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2323 BP; 680 A; 497 C; 609 G; 537 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression of REK7-binding activity. Primers based on isolated ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human foetal brain cDNA library, leading to the isolation of AL-1 cDNA (T18897). Sequence 4165 BP; 1157 A; 907 C; 1035 G; 1066 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse developmental kinase 1 MDK1 T2 clone. Mouse developmental kinase 1; MDK1 T2; rece RTK; signal transduction; probe; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegeneration; neuroproliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T32962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
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317. .2110
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03-JAN-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES FO
(SUGE-) SUGEN INC.
Clossek T, Millauer B,
                                                                                                                                                     T32960
T32960;
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CDNA cloning using adult mouse brains and Morthern blotting identified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that coded for truncated versions (M03422 and M03423, respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1 T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2901 BP; 890 A; 578 C; 650 G; 783 T;
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Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase;
RTK; signal transduction; probe; diagnosis; gene therapy;
neurodegeneration; neuroproliferation; cancer; ss.
                    Mouse developmental kinase 1 cDNA.
Mouse developmental kinase 1; MDK1; rec
signal transduction; probe; diagnosis;
neurodegeneration; neuroproliferation;
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A cDNA clone (T32960) codes for mouse developmental kinase 1 (MDK1) (M03421), a new member of the eck/eph family of receptor tyrosine kinases (RTKS). To isolate the clone, cDNA from mouse embryos was contificated to PCR amplification with primers based on conserved contificated to PCR amplification with primers based on conserved to screen an 11.5-day-old mouse embryo and an adult mouse brain cDNA ilbrary to obtain the MDK1 clone. 4 Sequence variants (see also T32961-62 and W03422-25) of MDK1 were also identified. MDK1 nucleic acids can be used for the recombinant prodn. of MDK1, as probes to detect MDK1, and for the gene therapy of diseases involving abnormalities in signal transduction, such as neurodegenerative and neuroproliferative disorders and cancer.

Sequence 4304 BP; 1297 A; 875 C; 1043 G; 1089 T;
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11-JUL-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES F
(SUGE-) SUGEN INC.
  US5814479-A.
29-SEP-1998.
11-JUN-1996;
04-JAN-1994;
                                                                                                                                                                                                                           25-NOV-1998 (first entry)

Mouse Bsk receptor-like tyrosine kinase; brain; diagnosis; leurodegenerative disease; limbic system neuron regeneration; chromosomal abnormality; degenerative growth; development disviral infection; bacterial infection; alzheimer's disease; epschizophrenia; stroke; cerebral ischaemia; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes mouse Bsk, which is a receptor-like tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in Bsk nucleic acid probes, which can be used in detecting alterations in the level of Bsk messenger-RNA (mRNA) in biological samples isolated from a mammal afflicted with a disease, such as neurodegenerative diseases or disorders and neoplasms. The nucleic acid sequence can also be delivered into the limbic system of patients with limbic system neuronregenerative disease, disorder or injury, to promote or enhance limbic system neuron regeneration or growth. Such neurodegenerative disease include, chromosomal abnormalities, degenerative growth and development disorders, viral infections, bacterial infections, brain schizophrenia, or stroke and cerebral ischaemia.

Sequence 4322 BP; 1260 A; 887 C; 1055 G; 1120 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KROM/) KROMER L F. (SCHU/) SCHULZ N T. (WOUD/) WOUDE G F V. (ZHOU/) ZHOU R. (ZHOU/) ZHOU R. Kromer LF, Schulz NT, VWPI; 98-541751/46.
Claim 2; Page 8-11; 18pp; English.

Two cDNA libraries were prepared, one from murine osteoblast-
cell line MC3T3-E1 and the other from mouse hepatic tissues.
stranded fragments of 300 bp were obtained using a random ext
primer and were blunt-ended. The ds linker ATOS-1/2 was ligat
the MC3T3-E1 cDNA and the ds linker ATOS-4/5 was ligated to 1
cDNA. PCR amplification of each product was
                                                                                                                                                                                            EP-614974-A.
14-SEP-1994.
28-FEB-1994;
10-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                         03/c
071303
071303;
                                                                                                                                                                                                                                                                                                                      Mouse osteoblast-specific osteoblast-specific factor bone metabolic disease; di
                                                                                                           New osteoblast specific control factor in bone f
                                                                                                                                                    (FARH ) HOECHST JAPAN LTD.
Amann E, Kawai S, Kikuno
WPI; 94-281204/35.
                                                                                                                                                                                                                                                                                           Mus musculus.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid sequence encoding protein - used in Bsk nucleic acid probes, used in detecting alterations in level of Bsk messenger-RNA in biological samples isolated from mammal afflicted
                                                                                                                                                                                                                                                                                                                                                              11-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                         cDNA to
                                                                                                                                                                                                                                                                                                                                   factor;
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                                                                                                            formation,
                                                                                                                                                                                                                                                                                                                   diagnosis; therapy;
                                                                                                                          factor
                                                                                                                                                                                                                                                                                                                                                                                         mRNA;
                                                                                                                                                                                                                                                                                                                                factor-6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB
Pred. No. 0.67
0; Mismatches
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                                                                                                           s - active used for
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                                                                                                                                                                                                                                                                                                                                 mouse;
                                                                 from murine osteoblast-like
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0.67;
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                                                                                                         as a transcription treating bone
                                                                                                                                                                Takeshita
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                        a random extension 1/2 was ligated to
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Matches 39
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Matches
                                                                                                                                                                                                           Claim 1; Page 41-45; 133pp; English.
Claim 1; Page 41-45; 133pp; English.
CDNAs (T02946-49) coding for 4 novel human EPH-like receptor protein
tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectivel
were isolated from a human foetal brain cDNA library using a directed
PCR approach with primers (see T02960-61) based on conserved regions
receptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show
extensive homology to the catalytic domain of chicken EPH-like
receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known
EPH-like receptor. The isolated cDNAs are used for prodn. of
recombinant HEKs and chimeric receptors, in hybridisation assays, and
to detect abnormalities in HEK receptor genes.
Sequence 2962 BP; 654 A; 914 C; 827 G; 567 T;
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Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Q71304) or ATOS-4 (Q71305), respectively. DNA specific for MC3TT-E1 was obtained by subtraction of sequences also found in liver library, then amplification with ATOS-1. This was a first step in the cloning procedure for isolating a MC3T3-E1 specific clone, coding for OSF-6 (see Q71303).

Sequence 2005 BP; 485 A; 534 C; 552 G; 434 T;
T02948 standard; cDNA;
T02948;
16-APR-1996 (first ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1402
                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
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15-APR-1994; US-229509.
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GM, Jing S, Welcher
95-373799/48.
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                                                                                                                                              37; Conservative
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1. .2913
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61.7%;
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; Pred. No. 7.3;
0; Mismatches
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No. 0.
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antibody; vector;
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12-OCT-1995: U04228.
04-APR-1995; US-222616.
04-APR-1994; US-222616.
(GETH) GENENTECH INC.
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26-OCT-1995.
14-APR-1995; UI
15-APR-1994; UI
(AMGE-) AMGEN
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Claim 1; page 57-62; 133pp; English.
Claim 1; page 57-62; 133pp; English.
cDNAS (T02946-49) coding for 4 novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively were isolated from a human foetal brain cDNA library using a directed PCR approach with primers (see T02960-61) based on conserved regions creceptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek7, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. The isolated cDNAs are used for prodn. of recombinant HEKS and chimeric receptors, in hybridisation assays, and
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Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOX GM,
WPI; 95
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Agonist antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extra domain and Ig constant domain, useful for studying, and then modulation of, cell growth and differentiation Disclosure, Page 88-92; 125pp; English.

DNA probes based on protein tyrosine-kinase (pTK) sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to detect abnormalities in HEK receptor genes. Sequence 3116 BP; 859 A; 720 C; 812
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                                                                                                                                             PSDB;
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95-366160/47.
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S, Welcher
                                                                                                                                                                                                                                                                                                                                                58. .29:
/*tag=
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58. .2958
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1. .57
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Pred. No. 8.8;
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bpTK7;
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AL035703 Human DNA L136642 Homo sapten AL121966 Homo sapt AC015609 Homo sapt AC021955 Homo sapt X91191 X.laevis mR L26099 Xenopus lae X78689 R.norvegicu

M68515 Mouse eph-r M68513 Mouse eph-r U69278 Rattus norv L36644 Homo sapien X95425 H.sapiens m U03910 Gallus gall U72207 Mus musculu

I68018 Sequence 9 M83941 Human recep M68514 Chicken eph I15007 Sequence 15 A28003 H.sapiens Description

AR062744 Sequence
AR025488 Sequence
AR002425 Homo sapi
Y14271 Gallus gall
AL138446 Homo sapi
U21955 Rattus norv
X79084 M.musculus
X79083 M.musculus
U21954 Rattus norv
U58332 Mus musculus
U201954 Rattus norv
U58332 Mus musculus
AC009491 Homo sapi
AC009496 Homo sapi
AC009497 Kanopus l
X65188 M.musculus
S57168 Sek-Eph-rel
AC015510 Homo sapi
AL109928 Homo sapi
AL109935 Mus musculu
U89295 Danio rerio
U73757 Mus musculu
U89295 Danio rerio
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1 (bases 1 to 3132)
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ISYPSHGWEETSGVDEHYTP IRTYQVCNYMDHSQNNWLERNWYPRNSAQKIYVELKFT
LRDCNSIPLYLGTCKETFULYYMESDDDHGVKFREQPTKIDTIAADESFTQMDLGDR
ILKLNYEIREVGPVNKAGFYLARQDVGACVALVSVRYYEKCPFTVKNLAMFPDTVPM
DSQSLVEVRGSCVNNSKEEDPRAYCSTEGEMLVPIGKCSCNAGYEERGFMCQACRAP
EYKALDGNMKCAKCPPHSSTQEDGSMNCFCENNYFRANDPFSAACTRPPSSPRNVIS
NINETSVILDMSWPLDTGGRKDVTFNIICKKCGMNIKQCEPCSPHVIFIKKORTSR
NINETSVILDMSWPLDTGGRKDVTFNIICKKCGMNIKQCEPCSPUTTIKKORTSR
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NSISLSWQEPEHPNGIILDYEVKYYEKCQETSYTILTARGTNVTISSLKPDTIYVLQ
IRARTAAGYGTNSKKFEETSDSFSISGESSQVYMIAISAAVAIILLTVVIYVLIGR
FCGYKKKHGADEKRLHEGNGHLKLPGLRTYVDPHTYEDPTQAVHEFAKELDATNISID
KVVGAGEFGEVCSGRLKLPSKKEISVAIKTLKVGYTEKQREDFLEASINGQFDHPNI
IRLEGYVTKSKFVMIVTEYMENGSLDSFLRKHDAQFTVLQLLGMLRGIASGMKYLSDM
GYVHRDLAARNILINSHLVCKYSDFGLSRVLEDDPEAAYTTRGGK IPROTSPEALIAY
RKFTSASDVMSYGIVLMEVMSVGERFYWEMSNQDVIKAAVDEGYRLPPPMDCPAALYQL
MLDCWGKDRNNRFKFEOIVSILDKLIRNFGSLKIITSAAARFSNLLLDQSNUD15TFR
TTGGMKLNGVRRAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKAL
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Location/Qualifiers
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/db_xref="GI:1247487"
/db_xref="SWISS-PROT:P29320"
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/db_xref="taxon:9606"
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1. 3132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 3149)
Wicks, I.P., Wilkinson, D., Salvaris, E. and Boyd, A.W.
Molecular cloning of HEK, the gene encoding a receptor tyrosine
kinase expressed by human lymphoid tumor cell lines
proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
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Human receptor tyrosine kinase (НЕК) mRNA, complete cds
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Homo sapiens lymphoid tumor cDNA to
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                       ISYPSIGWEELSGYDEHYTP IRTYQVCUMDHSQNUMLATINWVENSAQKIY VELKET
LRDONSIPLYLGTCKETFILY YMESDDDHGVKEREHQETKIDTI AADESETQMDLGDR
ILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYEKCPFTVKNLAMEPDTVPM
DSGSLVEVRGSCVNKKGFYLAFQDDFGACVALVSVRVYEKCPFTVKNLAMEPDTVPM
DSGSLVEVRGSCVNNKKEEDPPRMYGSTEGEFULPICKCSCNAGYEERGEMCQACRPG
FYKALDGNMKCAKCPPHSSTQEDGSMNCRCENNYFRADKDPSMACTRPPSSPRNVIS
NINETSVILDMSWPLDTGGRKDVTENIICKKCGWNIKQCEPGSPNVRELPRQFGLTNT
TVTVTDLLAHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPULTIKKDRTSR
NSISLSWQEPHPNGIILDYEVKYYEKQEQETSYTILAARGTNVTISSLKPDTIYVFQ
IRARTAAGYGTNSKKEFFETSPDSFSISGESSQVVMIAISAAVAIILLTVVIYVLIGR
FCGKKKHGADEKRLHERGNGHLKLPGLRTYVDPHTYEDDTQAVHEFAKELDATNISID
KVVGAGEEGEVCSGRUKLPSKKEISVAIKTLKVGYTEKQRRDFUGEASIMGQFDHPNI
IRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVQLVGMLRGIASGMKYLSDM
GYVHADLAARNILLNSNLVCKYSDFGLSRVLEDDPEAAYTTRGGKIPLRGTSPEAIAY
GYVHADLAARNILLNSNLVCKYSDFGLSRVLEDDDPEAAYTTRGGKIPLRGTSPEAIAY
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RKFTSASDVWSYGIVLWEVMSYGERPYWEMSNQDVIKAVDEGYRLPPPMDCPAALYQL
MLDCWQKDRNNRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLDQSNVDISTFR
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/protein_id="AAA58633.1"
/db_xref="GI:183932"
/translation="MCCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGW
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101. .3052
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101. .3052
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/db_xref="taxon:9606"
/cell_line="LK63"
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Sajjadi,F.G., Pasquale,E.B. and Subramani,S.
Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
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Gallus gallus
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Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                              YKASAGNYKCAKCPPHSSTYEDASINCRCEKNYFRSEKDPPSMACTRPPSAFRNYISN
INETSYILDWSWPLDTGGRKNYFRNIICKKCGGSSKICEPCSDAYRELPROTGLTNYT
YTVUDLLAHINYTFEIDAYNGYSDLSTISROFAAVSITTNQAAPSPITYIRKDRTSRN
SVSLSWQEPEHPNGIILDYEVKYYEKQEGETSYTILRAKSTNYTISGLKPDTTYPFQI
RAKRDAARYGTSSRKFEFETSPDSFSISSENSQYVMIAISAAVAIILLTVVVYVLIGRE
CGYKKSKHGTDEKRLHEGNGHLKLPGLRTYVDPHTYEDPNQAVHERAKELDASNISID
KVVQAGEFGEVCSGRLKLPSKKEISVAALKTLKAGYTEKQREDFLAGSIKGODHENI
IRLEGYVTKSKPYMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGMKYLSDM
GYVHADLAARNILIUMEVMSYGERFYWEMSFODVIKAVDEGYRLPPPMDCPAALYQL
MLDCWQKDRNNRPKFEQIVSILDKLIRWESSLKIITNAAARPSNLLLDQSNIDISAFR
TAGDWLNGFRFGQCKGIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIVSSIKTL
TRAGDWLNGFRFGGCKGIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIVSSIKTL
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                                                                                                                                                                                                                                                                                                         /product="receptor tyrosine kinase"
/protein_id="AAA4666.1"
/protein_id="AAA4666.1"
/protein_id="AAA4666.1"
/db_xref=="Gi:211447"
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RYPSHGWEEISGVDEHYPPIRTYGESNVMDH5QNMWLETWI IAADESGTIYVELKFTL
RDCNSIPLYLGTCKETPINLYWBSDDDHLAKFREHQFTKIDTIAADESFTVKNLAMFPDTVPMD
LKLNTEVREVGPYSKKGFYLAFGDVGACVALVSVRVYEKKCPFTVKNLAMFPDTVPMD
SQSLVETVREVGPVSKKGFYLAFGDVGACVALVSVRVYEKKGFTEGFACQACRPGF
VEAGANWCAGCONGGETTERACHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Cek4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gallus gallus"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Cek4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="10 day embryo"
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inae; Gallus.
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MUSMEK4SE
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I15007
I15007.1
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2032)
Sajjadi,F.G., Pasquale,E.B. and Subramani,S. Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
                                    g
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M68515
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Pasquale,E.B. and Sajjadi,F.G.
Eph-related tyrosine kinases, nucleotide sequences and methods
                                                                                                                                                                              receptor tyrosine kinase
Mus musculus (strain IRC
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                                                                                                                                                      Mus musculus
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    /organism="Mus musculus"

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737 c 796 g
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1. .3254
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93.9%;
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Pred. No. 7.3e
0; Mismatches
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Pred. No. 7.3e-13;
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.3e-13;
                                replaced gi:199121
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М68513.1
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Mouse eph-related
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Sajjadi, F.G., Pasquale, E.B. and Subramani, S.
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Mus musculus (strain IRC
                                                                                                                                                                                                                                                                   Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor new Biol. 3, 769-778 (1991)
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                                                                                 /gene="Mek4"
89. 30/0
                                                                                                                    /organism="Mus musculus"
/strain="IRC x Swiss Webster"
/db_xref="taxon:10090"
/dev_stage="11.5 day embryo"
/tissue_type="embryo"
89. .3040
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89. .170
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VTVTDLLAHTNYTFEIDAVNGVSELSSPPRQYAAVSITTNQAAPSPVMTIKKDRTSRN
SISLSWQEPEHPNGIILDYEVKYYQKQEQETSYTILRARGTNVTISSLKPDTTYVFQI
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SQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPPHSSTQEDGSMNCRCENNYFRAEKDPPSMACARPPSAPRNVISN
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2010. .2015
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AAA39521.1"
/db_xref="GI:199120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRDCNSIPLVLGTCKETFNLYYMESDDHGVKFREHQFTKIDTIAADESFTQMDLGDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDCHLSILVLLGCCVLSCSGELSPQPSNEVNLLDSKTIQGELGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Mek4 secreted"
/protein_id="AAA39522.1"
/db_xref="GI:454829"
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/dev_stage="11.5 day embryo"
/tlssue_type="embryo"
                                                                  /gene="Mek4"
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Pred. No. 5.3e-11;
0; Mismatches 7
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
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RNU69278
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ORIGIN
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                                                                                             Sg
                                                                                                                                      gene
                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 GTTAATCTACTAGATTCGAAAACAATTCAAGGAGAGCTGGGCTGGATCTCCTACCCATCC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 catggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

1 (bases 1 to 3077)

Li,Y.Y., McTiernan,C.F. and Feldman,A.M.

II-1 beta alters the expression of the receptor tyrgene r-EphA3 in neonatal rat cardiomyocytes

Am. J. Physiol. 274 (1), H331-H341 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
59; Conser
                                                                                                                                                                                                                                                                                                           Submitted (01-SEP-1996) Cardiology, University of Pittsburgh, Lothrop Street, Pittsburgh, PA 15213, USA On Apr 18, 1997 this sequence version replaced g1:1698721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNU69278 3077 bp mRNA ROD 23-MAR-1998 Rattus norvegicus eph-related receptor tyrosine kinase homolog (Rek4) mRNA, complete cds.

069278
                                                                                                                                                                                                                                                                                                                                                                                    Li,Y.Y., McTiernan,C.F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U69278.1 GI:1943913
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YTVTDLLAHTNYTFEIDAVNGVSELSSPRQYAAVSITTNQAARSPYMYIKKDRTSRN
SISLSWQEPEIB NGILLDYEVKYYRKQEDETSYTILRARGTNVTISSLKRDTTYVFQI
RARTAAGYGTNSRKFEFETSPDSFSISGENSHVVMIAISAAVAIIVLTVVTYVLVGRF
GGYHKSHSAEEKRLHFGNGHLKLPGLKTYVDFHTYEDPTQAVHEFAKELDATNISI
KVVGAGEFEGVSGKLKLPSKKEISVAAKTLKGYTEKORRDFLGEASIMGOPDHPNI
IRLEGVVTKSKPEMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGMKYLSDM
GYVHRDLAARNILINSNLFCKVSDFGLSRVLEDDPEAAYTTRGGRIPHRWTSPEAMSY
RKFTSASDVWSYGIVLMEVMSYGERYFSOMSNODVIRAVDETKRPPDMCPBALYQL
MLDCWOKDRNNRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLDQSNVDIATFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRDCNSIPLVLGTCKETFNLYYMESDDHGVKFREHQFTKIDTIAADESFTQMDLGDRI
LKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPETVKNLAMFPDTVPMD
SQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCTCNAGYEERGFICQACRPGF
                                                                                             /gene="Rek4"
35. .2989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKASDGAAKCAKCPPHSSTQEDGSMNCRCENNYFRAEKDPPSMACARPPSAPRNVISN
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ISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFT
/gene-"Rek4"
/codon_start-1
/product-"eph-related receptor tyrosine kinase homolog"
/protein_id-"AACO6273.1"
                                                                                                                                                           /cell
                                                                                                                                                                                /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/dev_stage="neonatal"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                           .3077
                                                                                          .2989
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                                                                                                                                                         _type="cardiomyocytes"
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Pred. No. 5.5e
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                           and Feldman, A.M.
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5.5e-11;
hes 7;
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Rattus.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L36644.1 GI:551611

EPH-like receptor PTK; receptor protein-tyrosine kinase.

Homo sapiens (clone library: Stratagene premade library, cat
#936206) female fetus, 17-18 weeks gestation brain cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens receptor protein-tyrosine kinase (HEK7) mRNA, 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor protein-tyrosine kinases
Oncogene 10 (5), 897-905 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA cloning and tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3162)
Fox,G.M., Holst,P.L., Chute,H.T., Lindberg,R.A., Jan Basu,R. and Welcher,A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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IRARTAAGYGTNSRKFEEENSEDSFSISGENSHVMIAISAANAIIVLTYVTYVLVGR
FCGYHKSKHSSDEKRLHEGNGHLH-PGLATTYDPHTYEDPTAAVHEFAKELDATNIAI
DKVVGAGEFGEVCSGRLKLPSKKEISVALKTLKVGYTEKORRDFLGEASIMGQFDHPN
IIRLEGYVTKSKPVMIVTEYMEMGSLDSFLRKHDAQFTVIOLVGMLRGIASGKYLSD
MGYVHRDLAARNILINSNLVCKVSDEFGLSKVLEDDPEAAYTTRGGKIPVMTSPEATA
YRKFTSASDVWSYGIVLMEVMSYGERFYWEMSNQDVIKAVDEGYRLPLPMDCPAALYO
LMLDCWGKDRNMEPKFEDIVSILDKLIRNPGSLKIITSAAARPSNLLLDOSNVDIATE
LMLDCWGKDRNMEPKFEDIVSILDKLIRNPGSLKIITSAAARPSNLLLDOSNVDIATE
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/translation="MDCHLSLITEGCCVLSCSRELSPOPSNEVNLLDSKTIQGELGW
/translation="MDCHLSLITEGCCVLSCSRELSPOPSNEVNLLDSKTIQGELGW
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ILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPM
DSQSLVBVRGSCVNNSKEEDPPRMYCSTEGEMLVPIGKCTCNAGYEERGFICQACRPG
EYKALDGVAKCTKCPFHSSTQEDGRMNCRCEMNYFRAEKDPBMACTRPPSAPRNVIS
NINETSVILDWGWPLDFGGRKDITFNIICKKCGWNVRQCEPCSPNVRFLPRQLGITNT
TVTVPDLLAHNNYTFEIDAINGVSELSSPPRGFAAVSITTNQAAPSPYMTIKKDRTSR
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714 c
                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="fetus, 17-18 weeks gestation"
/codon_start=1
/product="receptor protein-tyrosine
/protein_id="AAA74245.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTTGDWLNGMRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKA
                                                                                                                           /gene="HEK7"
                                                                                                                                                                                                                                                   /clone_lib="Stratagene premade library, cat #936206"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                         gene-"HEK7"
                                                                                                                                                                          product="receptor protein-tyrosine kinase"
                                                                                                                                                                                                       /gene="HEK7"
                                                                                                                                                                                                                                                                                                             /sex="female"
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Pred. No. 2.3e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of five human EPH-like
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REFERENCE AUTHORS

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ACCESSION DEFINITION LOCUS

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                                                                                                                                                                                   Submitted (26-JAN-1996) Guido C. Miescher, University Hospitals Basel, Department of Research, Departement Forschung, Kantonsspit Basel, 4031 Basel, Switzerland Overlaps with L36642-L36645
Partial human EHK-1 cDNA without information on mRNA splicing variants has been published by Fox, G.M. et al. (1995). Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                            Extensive splice variation and localization of the EHK-1 receptor tyrosine kinase in adult human brain and glial tumors Brain Res. Mol. Brain Res. 46 (1-2), 17-24 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSEHK1 3903 bp mRNA
H.sapiens mRNA for EHK-1 receptor
X95425
X95425.1 GI:1177465
                                                                                                                                                                    variants has been published by 10:897-905.
                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                          Miescher Constant, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miescher, G.C., Taylor, V., Olivieri, G., Mindermann, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           97334377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Steck, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHK-1; receptor tyrosine kinase
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RQSGLKNTSVMMVDLLAHTNITFEIEAVNGFARQYGVEARQYGVETTRQAABSSVTIN
VKKGKIAKNSISLSWQEDDRPNGIILEYEIKHDESCHARQYGVTIIKSKETITABGLKF
VKKGKIAKNSISLSWQEDDRPNGIILEYEIKHDESCHOETSYTIIKSKETITABGLKF
ASVYVFQIFARTAAGYGVFSRRFEFETTPVFAASSDQSQIPVIAVSVTVGVIILLAVVI
GVLLSGREGCGYSKAKQDPEESKHFHHGHIKJPGVRTIIDPHTYETKORNQAVHEEAKEI
EASCITIERVIGAGEFEGEVCSGRLKLJPGKRELLAVAIKTIKVGYTEKORNDFIGEASKI
EASCITIERVIGAGEFEGEVCSGRLKLJPGKRELLAVAIKTIKKOYTEKORNDFIGEASKI
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TAPEAIAFRKFTSASDVWSYGIVMWEVVSYGERPYWEMTNQDVIKAVEEGYRLPSPMD
CPAALYQLMLDCWQKERNSRPKFDEIVNMLDKLIRNPSSLKTLVNASCRVSNLLAEHS
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FPDTITGADSSQLLEVSGSCVNHSVTDEPPKMHCSAEGEWLVPIGKCMCKAGYEEKNG
TCQVCRPGFFKASPHIQSCGKCPPHSYTHEEASTSCVCEKDYFRRESDPPTMACTRPP
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/clone_lib="lambda ZAPII #936206"
/clone="HFB415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HEK7"
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VMGDLGWIAFPKNGWEEIGEVDENYAPIHTYQVCKVMEQNQNNWLLTSWISNEGASRI
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                                                                                                                                           ocation/Qualifiers
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RESULT 11
GGCEK7B
LOCUS
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ORIGIN
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Best Local Similarity
Matches 46; Conserv
      AUTHORS
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                                                                                                                                                                                         GGCEK7B 4124 bp mRN1
Gallus gallus receptor-type
(Cek7) mRNA, complete cds.
Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 4124) Siever, D.A. and Verderame, M.F.
                                                                                                                                                     U03910.1
                                                                                                           chicken.
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KDQETESTIIKSKETTITAEGLKPASVYVFQIRARTAAGYGVESTIIKSKETETTPYTAAS
SDQSQIPVIAVSVTVGYLLLAVVIGVLLSGSCCECGCGRASSLCAVAHFILIWRCGYS
KGACDPEEEKMHFHNGHIKLPGVRTYIDPHTYEDPNQAVHEFAKEIEASCITIERVIG
AGEFGEVCSGRLKLPGKRELPAIKTLKVGYTEKQRDFLGEASIMGQTDHPNIIHLE
GVYTKSKPVALYTEYKENGSLDTFLKKNDGDFTPIQLAVGALRGISAGKKYLSDMGYVH
RDLARNILINSNLVCKYSDFGLSRVLEDDPEAAYTTRGGKIPIRWTAPEAIAFRKFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="RNA splice domain IIa"
2114. .2392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAEGEWLVPIGKCMCKAGYEEKNGTCQVCRPGFFKASPHIQSCGKCPPHSYTHEEAST
SCVCEKDYFRRESDPPTMACTRPPSAPRNAISNVNETSVFLEWIPPADTGGRKDVSYY
IACKKONSHAGVCEECGGHVRYLPRQSGLKNTSVMVDLLAHTNYTFEIEAVNGVSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLCAALRTLLASPSNEYNLLDSRTVMGDLGWIAFPKNGWEEIGEVDENYAPIHPYQVC
KVMEQNQNUMLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFMNYYFESDD
QNGRNIKENQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG
ACIALVSVRVYYKKCPSVVRHLAVFPDTITGADSSQLLEVSGSCVNHSVTDEPPKMHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="RNA splice domain IIb"
2502. .2567
/note="RNA splice domain III"
882 c 953 g 977 t
                                                                                                                                                       GI:555617
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WQKERNSRPKFDEIVNMLDKLIRNPSSLKTLVNASCRVSNLLAEHSPLGSGAYRSVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="EHK-1 receptor tyrosine kinase"
/protein_id="CAA64700.1"
/db_xref="GI:1177466"
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/clone="HFB129"
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/cell_type="CNS neurons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MRGSGPRGAGHRRPPSGGGDTPITPASLAGCYSAPRRAPLWTCL"
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MEDLINE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of a complete Cek7 receptor protein tyrosine kinase coding sequence and cDNAs of alternatively spliced transcripts Gene 148 (2), 219-226 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Siever, D.A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="receptor-type protein-tyrosine kinase"
/product="receptor-type protein-tyrosine kinase"
/protein_id="RAB60614.1"
/db_xref="G1:55620"
/db_xref="G1:55620"
/transiation="MGLEGGGRAGGPAPGWTCLLCAALRSLLASPGSEVNLLDSRT
/VMGDLGWIAYPKNGWEEIGEVDENYAPIHTYQVCKVMEDQNNWLLTSWISNEGRRAS
SFELKFTLRDCNSLPGGLGTCKETFNMYFESDDEDRINERQYIKIDTIAADESFT
ELDLGDRVMKLMTEVRDVGPLTKKGFYLAFQDVGACIALVSVRVYYKKCPSVIRNLAR
FPDTITGADSSQLLEVSGVCVNHSVTDEAPKMHCSAEGEWLVPIGKCLCKAGYEEKNN
TCQAPSTVSSVKKGKITNASISLSWQEEDRPWILILLYFENDOGGTSYTIIKSKE
TAITADGLKPGGAYVFQIRARTAAGYGGESTRREEFETSPVLAASSQSQOLPITVSVT
VGVILLAVVIGFLLSGRRCGYSKAKQDPEEEKMHFHNGHIKLPGVRTYIDPHTYEDPN
QAVHEEAKEIEASCITLERVIGAGEFGEVGSGLKLQGKREEFPVAIKTLKVGYTEKQR
RDFLGBASIMGGOHPNIIHLEGVYTKSKEVMHTVETMENGSLDTFLKKNDGOFTVIQ
LVGMLRGIASCHKYLSDMGYVHADLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYT
TRGGKLPIRMTAPEALAFRKFTSASDVWSYGIVMEVMSYGERFYWEMTNODVIKAVE
TRGGKLPIRMTAPEALAFRKFTSASDVWSYGIVMEVMSYGERFYWEMTNODVIKAVE
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/db_xref="taxon:9031"
/clone-"overlapping clones: 1-13, 2-6, and 9-13"
/tissue_type="body wall"
/dev_stage="ten-day embryo"
/note-"this sequence diverges 3' of nucleotide 3023 when compared with previously reported Cek7 sequence (GenBank Accession Number Z19058)"
SAPRSAISNIVNETSVELEMITPADTGGRKDVSYYIACKKCNSHSGLCEACGSHVRYLD
QQTGLKNTSVMAVDLLAHTNYTEIEAVMGVSQNYGARQFVSVNYTTRQAAPSPVSS
VKKGKITKNSLSLSWQEPDRENGIILEYEIKY EEKOQETSYTIIKSKETAITADGLKG
GSAYVFQIRARTAAGYGGFSRRFEEFETSPVLAASSDQSQIPIIVVSVTVGVILLAVVI
GFLLSGSCCDHGCGWASSLRAVAYSCITIERYLGAGEFEGEVCSGRLKLOGKREEPPAL
KTLKVGYTEKQRRDFLGEASIMGQFDHPNIIHLEGVVTKSKPVMIVTEYMENGSLDTF
                                                                                                                                                                                                                                     ELDLGDRYMKLNTEVRDYGPLTKKGFYLAFQDYGACIALVSVRYYYKKCPSVIRNLAR
FPDTITGADSSQLLEVSGYCVNHSYTDEAPKMHCSAEGEWLVPIGKCLCKAGYEEKNN
TCQYCRPGFFKASPHSPSCSKCPPHSYTLDEASTSCLCEEHYFRRESDPPTMACTRPP
                                                                                                                                                                                                                                                                                                                                           /translation="MGLRGGGGRAGGPAPGWTCLLLCAALRSLLASPGSEVNLLDSRT
VMGDLGWIAYPKNGWEEIGEVDENYAPIHTYQVCKVMEQNQNNWLLTSWISNEGRPAS
SFELKFTLRDCNSLPGGLGTCKETFNWYYFESDDEDGRNIRENQYIKIDTIAADESFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVTLVGHQKKIMNSLQEMKVQLVNGMVPL" 85. .3126
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RVSNLLVEHSPVGSGAYRSVGEWLEAIKMGRYTEIFMENGYSSMDSVAQVTLEDLRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="receptor-type protein-tyrosine kinase"
/protein_id="AAB60612.1"
/db_xref="GI:555618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Cek7"
/codon_start=1
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(insertion A) and nucleotides 1802-1867 (insertion B)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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VMGDLGWIAFPENGWEEIGEVDENYAPIHTYQVCKVMENQNNWLLTSWISNEGREAS
SFELKFILROCNSLPGGLGTCKEIFNMYFPESDDEGNIRENQTIK IDTIAADESFT
ELDLGGDRVMKLMTEVROVGFLTKKGFYLLAFQDVCACIALVSVRVYKKCPSVIRNLAR
FPDTITGADSSQLLEVSGVCVNHSVTDEAPKMCSAEGEWLVPIGKCLCKAGYEEKNN
TCQVCKPGFFKASPHSPSCSKCPPHSYTLDEASTSCLCEENYFRRESDPTMACTRP
SAPRSALSNVMETSVFLEWIFPADTGGRKDVSYIACKKCNSHSGLCEACGSHVRYLP
QQTGLKNTSVMAVDLLAHTNYTEFIEAVKGVSDQNFGARQFVSVNVTTNQAAPSPVSS
VKKGKITKNSISLSWQEEDRPNGIILEYEIKYFEKDQETSYTIKSKETALTADGLKP
GSAYVFQIRAFTAAGYGGFSRRFEFETSFVLAASCAQPPITIKSKETATADGLKP
GSAYVFQIRAFTAAGYGGFSRRFEFETSFVLAASSDQQIPIIVSVTVGVILGAASI
EASCITIERVIGAGEFGEVCSGRLKLQGKREFFVAIKTLKVGYTEKQRDFLGEASIM
GQFDHFNIIHLEGVYTKSKFVMIVTEYMENGSLDTFLKKUDGQFTVIQLVGMLRGIAS
GMKYLSDMGYVHRDLAARNILINSMLVCKVSDFGLSRVLEDDPBAAYTTRGGKIPIKM
TAPEALAFKFTSASDVWSYGITWMEVMSYGERFWEMTWQDVIKANSEGYRLLPSPMD
CDAALYQLMLDCWGKDENSRPKDDEIVSMLDKLLRNPSKLTLVARSSRYSNLLVEHS
CDAALYQLMLDCWGKDENSRPKDDEIVSMLDKLLRNPSKLTUVARSSRYSNLLVEHS
CDAALYQLMLDCWGKDENSRPKDDEIVSMLDKLLRNPSKLTUVARSRYSNLLVEHS
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                                                                                                                                                                                                                                              /gene="Cek7"
/note="hydrophobic region characteristic of transmembrane domain"
3127. .4174
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/product="protein-tyrosine kinase precursor"
85. .177
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/note="polymorphism
does not alter the a
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IMNSLQEMKVQLVNGMVPL"
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EMTNQDVIKAVEEGYKLPSPMDCPAALYQLMLDCWQKDKRFKPEDEIYSMLDKLIRN
PSSLKTLVNASSRVSNLLVEHSPVGSGAYRSYGEWLBALKMGRYTEIFMENGYSSMDS
VAQVTLEDLRRLGVTLVGHQKKIMNSLQEMKVQLVNGMVPL"
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/protein_id="AAB60613.1"
/db_xref="GI:555619"
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1726. 1797
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does not alter the amino acid sequence"
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                                                                         catggg
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Submitted (23-SEP-1996) Molecular Oncology,
P.O. Box 4000, Princeton, NJ 08543, USA
Location/Qualifiers
                                                                                                                                                             L Similarity
45; Conserva
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Eutheria; Rodentia;
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GADSSSLVEVRGQCVRHSEERDĪPKMYCSAGGGWLVPIGKCVCSAGYEERDJACMACE
LGFYKSARGDQLCARCPHSHSATPFAAQTCRCDLSYVRALDDPPSAACTRFPSAAPNL
ISSVNGTSVILLEWAPPLDPGGRSDITYNAVCRRCPWALSHCEACGSGTRFVPQQTSLA
QASLLVANLLAHMYSEWIEAVVGVSNLSPEPRSAVVNITTŅOAAPSQVVVLRQERA
GQTSVSLLWQBEBEQPNGILIEXFEIKYYEKDKEMOSYSTLKAVTTRATVSGLKPGTRYV
FQVRARTSAGCGRFSQAMEVPETGKPFPXDTRTIVWICLTLITGLVVLLLLLICKKH
CGYSKAFQDSDEEKMHYQNGQAPPVFLPLNHPPKFPTGPFAFPTYEFGRAGRG
FTREIEASRIHIEKIIGSGESGEVCYGRLQVFOQRDVPVAIKALKAGYTERQRODFLS
EAAIMGQTDHPNIIRLEGVVTRGRLAMIVTEYMENGSLDAFLRTHDGQFTIVQLVGML
RGVGAGMRYLSDLGYHRDLAARNULVDGRLVCKVSDFGLSRALEDDPEAAYTTAGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mapararlspalwvvtaaaaatcvsagrgevnildtstihgdwg
wltypahgwdsinevdesfrpihtyQvcnvmspnQnnwlrtnwvprdgarrvyaeikf
tlrdcnsipgvlgtcketfnlhyLesdrdlgastQesQflkiDTiaadbsftgablgv
                                                                                                                                                                                                                                                                                GITLMGHQKKILGSIQTMRAQLSSTQGRRRHL"
1504 c 1381 g 881 t
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PAPWGCPRALHQLMLDCWHKDRAQRPRFAHVVSVLDALVHSPESLRATATVSRCPPPA
FARSCFDLRAGGSGNGDLTVGDWLDSIRMGRYRDHFAAGGYSSLGMVLRMNAQDVRAL
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/product="Eph-and Elk-related kinase"
/prottein_id="AAB39218.1"
/db_xref="GI:1750259"
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79. .3093
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Sciurognathi; Muridae; Murinae;
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                                                                                                                                                        Score 32.4; DB 12;
Pred. No. 0.033;
0; Mismatches 21;
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On Nov 15, 1999 this sequence version replaced g1:6114770.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
RP1-61A9 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pleter de Jong. For further details see http://bacpac.med.buffalo.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is the entire insert of clone RP1-61A9
Location/Qualifiers
/note-"Tandem repeat. Forced join. G. Restriction digest to be 1200-1500bp complement(82130. 82878) /note-"match: GSS: Em:AQ750854.1" complement(82496. 82871)
                                                                                                                                 /note="match: GSS: Em:AQ816982.1"
complement(51292)
                                                                                                                                                                                                                                                                                               /note="match: GSS: 29241. .29448
                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:AQ010082"
25683. .25889
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(939. .1245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="p35.2-36.13"
/clone="RP1-61A9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organ1sm="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .160703
                                                                                                                                                                                                         /note="Single clone region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160703 bp
                                                                                                                                                                                                                                                                      'note="Weak
                                                                                                                                                                                                                                                                                                                                                                                                                              note="match: GSS: Em:AQ134928"
                                                                                                                                                                                                                                                                                                                                                                                                        .9888
                                                                                                                                                                                                                                                                   Data"
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clone RP1-61A9 on
                                                                                                                                                                                                                                                                                                                        Em: AQ594605.1"
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                                                                                                      Gap sized
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BASE COUNT
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                                                                 SOURCE
                                                                                                                                                                            HUMRPTK
                                                                                                                                                                                           RESULT
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Best Local Similarity
Matches 45; Conserv
                                   ORGANISM
                                                                                                                                                                                                                                                                                                    59996 GTGAATTTGCTGGACACGTCGACCATCCACGGGGACTGGGGTTGGCTCACGTATCCGGCT 59937
                                                                                                                                                                                                                                       59936 CATGGG
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                                                               EPH-like receptor PTK; receptor protein-tyrosine kinase.
Homo sapiens female fetus, 17-18 weeks gestation brain cDNA to
                                                                                                                                           Homo sapiens receptor
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                  Homo sapiens
                                                                                                L36642.1
                                                                                                              L36642
                                                                                                                             complete cds.
                                                                                                                                                             HUMRPTK
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82591. .82878
/note="match: 0
86392. .86712
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complement(152202.
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Complement(138397. 138744)

/note="match: GSS: Em:AQ504997.1"

complement(138398. 138763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: GSS: Em:AQ746639.1

Complement(13895. 138703)

/note="match: GSS: Em:AQ214151"

complement(138397. 138766)
                                                                                              GI:551607
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complement(121941.
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139243. .139556
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138774. .139225
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138773. .1392
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130586. .131194
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/note="match: G:
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126867. .127465
/note="match: GSS: Em:AQ419366"
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126813. .127149
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126892. .127225
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                                                                                                                                                            4523 bp
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                                                                                                                                                                                                                                                                                                                                                             Score 32.4; DB 10;
Pred. No. 0.044;
0; Mismatches 21;
                                                                                                                                          mRNA PRI 10-AUG-1995
protein-tyrosine kinase (HEK11) mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Em: AQ479682.1"
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RESULT 15
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AUTHORS
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MEDLINE
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                                               ORGANISM
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nes 42; Conserv
                                                                                                                                                                                                                                                                                                                               CTGCTGGATTCTAAAGCACAACAAACAGAGTTGGAGTGGATTTCCTCTCCACCCAATGGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases Oncogene 10 (5), 897-905 (1995) 95206782
                                                                                                                                                   HSJ189K14 116490 bp DNA
Homo sapiens chromosome 6 clone R
PROGRESS ***, 6 unordered pieces.
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Fox, G.M., Holst, P.L., Ch
Basu, R. and Welcher, A.A.
                                                                                                            AL121966.1 GI:6981849
                                                                                                                                                                                                HSJ189K14 116490 bp
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                             Homo sapiens
                                                                                      HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1447
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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TGLEDNYTVMDLLAHANYTEEVEAVNGVSDLSRSQLEPAVSITTGQAAPSVGSVM
KERVLQRSVELSWQEPEHPNGVITEYEIKYYEKDQRERTYSTVKTKSTSASINNLKSG
TYYVEQIRAFTAAGYGNYSPRLDVATLEEATGKMFEATAVSSEQNPVIIIAVVAVAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERKMKLNTEVREIGPLSKKGFYLAFQDVGACIALVSVKVYYKKCWSIIENLAIFPDT
VTGSEFSSLVEVRGTCVSSAEBEAENAPRMHCSAEGEWLVPIGKCICKAGYQQKGDTC
EPCGRGFYKSSSQDLQCSRCFTHSFSDKEGSSRCECEDGYYRAPSDPPYVACTRPPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYWDMSNQDVIKAIEEGYRLP
APWDCPAGLHQLMLDCWQKERAERPKFEQIVGILDKMIRNPNSLKTPLGTCSRPISPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IILVFMVFGFIIGRRHCGYSKADQEGDEELYFHFKFPGTKTYIDPETYEDPNRAVHQF
AKELDASCIKIERVIGAGEFGEVCSGRLKLPGKRDVAVAIKTLKVGYTEKQRRDFLCE
ASIMGQFDHPNVVHLEGVVTRGKPVMIVIEFMENGALDAFLRKHDGQFTVIQLVGMLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HQKKIMSSIQTMRAQMLHLHGTGIQV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="receptor protein-tyrosine kinase"
/protein_id="AAA74243.1"
/db_xref="GI:551608"
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186. .3182
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LEWISSPPNGWEEISGLDENYTPIRTYQVCQVMEPNQNNWLRTNWISKGNAQRIFVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="HEK11"
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/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JDQNTPDFTTFCSVGEWLQAIKMERYKDNFTAAGYNSLESVARMTIEDVMSLGITLVG
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Pred. No. 0.097;
0; Mismatches 18;
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                                                                                                                                                                          NA HTG
clone RP1-189K14,
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                                                                                                                                                                                                                                                                                                                                                                                             Indels
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QUENCING IN
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ORIGIN
Search completed: May 15, Job time: 18621 sec
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JOURNAL
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Best Local Similarity
                                                                                                                                                                                                                                 Matches
                                                                                                                              15905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                   AL Submitted (16-OCT-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 16, 2000 this sequence version replaced gi:006105.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of seqments is not known; 800 n's separate
segments. Unfinished: dJ189K14 Contig_ID: 00235
Length: 4081 bp Unfinished: dJ189K14 Contig_ID: 00235
acc=AL121966 Length: 19639 bp Unfinished: dJ189K14 Contig_ID: 00370
acc=AL121966 Length: 26994 bp Unfinished: dJ189K14
Contig_ID: 00919 acc=AL121966 Length: 31021 bp Unfinished:
dJ189K14 Contig_ID: 01165 acc=AL121966 Length: 29139 bp
Unfinished: dJ189K14 Contig_ID: 01338 acc=AL121966 Length: 1616
                                                                                                                           CTGCTGGATTCTAAAAGCACAACAAACAGAGTTGGAGTTGCATCTCTCCTCCACCCAATGGG 15964
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24521 25320; gap of
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25321 52314; contig of 26994 25
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84135; contig of 31021 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                       37770
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4082 4881: gap of 800 bp
4882 24520: contig of 19639 bp in length
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/clone_lib="RPCI-1"
18571 c 20111 g
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/db_xref="taxon:9606"
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70.08;
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Copyright (c) 1993 - 2000
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Result
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50: gb_est31: *
51: gb_est32: *
52: em_est32: *
53: em_est32: *
54: em_est22: *
55: em_est23: *
56: em_est23: *
56: em_est24: *
56: gb_est34: *
66: gb_est34: *
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68: em_est29: *
69: gb_est34: *
69: gb_est44: *
69: gb_gss3: *
69: em_gss4: *
69: gb_gss3: *
69: em_gss4: *
69: gb_gss3: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

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KEYWORDS
SOURCE
ORGANISM
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VERSION
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                                                                        AUTHORS
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                                                     TITLE
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                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mai
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
E 1 (bases 1 to 835)
S Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A.,
Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a mouse brail
library made by oligo-capping method
Unpublished (1999)
Un May 18, 1998 this sequence version replaced gi:3137;
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
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5', mRNA sequence.
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                                                                                                                                                                                mncb
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                     replaced g1:3137227.
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cDNA clone MNCb-6241
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AIO11632 EST206083
AIO11632 EST206083
AIS219 yf80812.r1
AI325344 m101c02.x
AIA19967 qx47402.x
AIA193334 m101c02.x
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AII32334 f132f03.s1
AW233440 f132f03.s1
AW233440 f132f03.x1
AW23340 f132f03.x1
AW23340 f132f03.x1
AII379458 f146608.y
AII079781 AW25667 DKFZP434N
AII079781 DTCSSCPPhil
AII67989 wJ01d11.x
AII107981 DTCSSCPPhil
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AII1079481 DTCSSCPPhil
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AII112817 H2CSSCPPhil
AW25663 EST304800
AII66919 qy94h06.x
AII112817 UI-R-Y0-m
AL036415 CIT-HSP-2
AA967414 ua65602.r
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B36983 HS-1042-A
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Best Local Sin
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                                                                                                                                                                           aatgtcatggaccacagtcaaaacaattggctgagaacaaactgggtccccaggaactca 120
                                                                                                                                                                                                                                                                                                                                                                                                   tgggaagagatcagtggtgtggatgaacattacacacccatcaggacttaccaggtgtgc
                                                             tttccagacacggtacccatggact----cccagtccctggtggaggttagagggtctt
                                                                                                                                                                                                                                ggggtgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt 300
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          GNGTNAACNACTNANAAAAAAGGATGNGCCNAAAATGNNCTGNGGGGCNNANGGNNANG
                            gtgtcaacaattctaaggaggaagatcctccaaggatgtactgcagtacagaaggcgaat
                                                   TTTCCTGATACCATTACTGGGGGGCTGATACCCTCTTNCCTGGNGGAAGTTCNAGGCTCCT
                                                                                            CTGGTGTCTGTCCNTGTGTTCTACAANAAGTGNCCACTTNCCCGTTCNAAATTANCCCAN
                                                                                                       ttggtgtctgtgagagtatacttcaaaaagtgcccatttacagtgaagaatctggctatg
                                                                                                                                    GGGCCACTGAGCAAGAAAGGGTTTTACCTGGCTTTTCAGGATGTGGGTGCTTGCATCGCC
                                                                                                                                                99tcctgtcaacaagaagggattttatttggcatttcaagatgttggtgcttgtgttgcc
                                                                                                                                                                                                                      GAGCGCTTCATCAGAGAGAGCCAGTTTGGCAAGATCGACACCATCGCAGCTGATGAGAGC
                                                                                                                                                                                                                                                              GTCATGGGGACTTGCAAGGAGACGTTTAACCTCTACTACTATGAGTCGGACAACGACAAG
                                                                                                                                                                                                                                                                                                       GCGCAGAGGGTGTACATTGAAATTAAGTTCACTCTAAGGGACTGCAACAGTCTTCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-Ku, Tokyo 162-8640, Japan
23-1, Toyama 1-chome, Jp
Email: khashlenih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was
ligated to a DrailI adaptor [TGTTGGCCTACTGG], digested
and cloned into dstinct DrailI sites of the pME18S-FL3.
XhoI sites just outside the DrailI sites can be used to
isolate the cDNA insert. Size selection was performed to
exclude fragments <1.5 kb. Library was constructed by
Sugano et al. (University of Tokyo, Institute of Medical
Science). Custom primer for sequencing: 5' end primer
[CTTCTGCTCTAAAACCTGCG]"
02 a 182 c 230 g 190 t 31 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_11b="Sugano mouse brain mncb"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="MNCb-6241"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ://www.nih.go.jp/yoken/genbank/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 276.6;
Pred. No. 6.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
Insert Size: 2663
High quality sequence stops: 276
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2663 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
On May 5, 1995 this sequence version
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yp50g04.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190902 5' similar to gb:M83941 TYROSINE-PROTEIN KINASE RECEPTOR HEK PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 276.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H38363.1 GI:907862
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                                                                                                      109
      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:3847311"
/db_xref="taxon:9606"
/clone="IMAGE:190902"
                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="retina"
                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares retina N2b4HR"
                    30.4%;
   0
Score 200.6; DB 23; Pred. No. 1.3e-48; 0; Mismatches 7;
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                                 Length 435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra Hilier,L., Clifton,S., Allen,M., Gibbons,M., Johnson,J., Gibbons,M., Johnson,J., Gibbons,M., Johnson,J., Bowers,Y., Wylie,T., Waterston,R. and WashU Zebrafish EST Project 1999
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi Other_ESTs: fi31907.x1
Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gttttaggaacttgcaaggagacattcaac 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library constructed by Dr. Sumio Suga
Sequencing by: Washington University
Seq primer: T3 ET from Amersham
High quality sequence stop: 485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 572)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRECURSOR ;, mRNA sequence.
/note="vector: pME185-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sundo Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Koichi Kawakami. Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                                                                                                                                                                                                                                                                                                                                 /clone_lib="Sugano Kawakami zebrafish DRA"
/sex="mixed (one male and one female, incluunfertilized eggs)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="AB"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (phage resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="2639282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Jniversity Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    St. Louis, MO 63108, USA
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JOURNAL COMMENT
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SOURCE
ORGANISM
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                                                                                                                      Tagged Connectors
Unpublished (1997)
Contact: Mahairas GG, Zackrone KD,
University of Washington
Seattle, WA 98195, USA
Tel: (206) 618-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGCGATACATCCGAGAAAAACCAGTTCACCAAAATCGACACCATTGCAGCTGATGAAAG
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                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 424)

Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood, L.E. Construction of a Characterized Clone Resource for Genomic Sequencing; Generation and Preliminary Analysis of 20,000 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
B36983
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HS-1042-A2-F05-MR.abi
sapiens genomic clone
                                                                                 Sequence Tagged Connector Plate: CT 824 row: K co
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a 136 c 160 g 104 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=CT 824 Col
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70.8%;
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Best Local Similarity
Matches 233; Conserv
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                                                                                                                                The Institute for Genomic Research 9712, Medical Center Drive, Rockville, Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIO11631 474 bp mRNA EST206082 Normalized rat ovary, ROVAX55 3' end, mRNA sequence.
                                                                                                                                                                                                                                                        Unpublished (1998)
On Jan 19, 1998 this sequence
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Lee, N.H., Glodek A., Chandra, I., Mason, T.M.,
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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E-Coli DH10B"
a 77 c 101 g
         /organism="Rattus sp."
/db_xref="ATCC (inhost):2021827"
/db_xref="taxon:10118"
/db_xref="taxon:10118"
/clone="8p0xX55"
/clone=1ib="Normalized rat ovary, Bento Soares"
/note=""organ: ovary; Vector: pT7T3Pac; Site_1: 1
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Pred. No. 8.9e-32;
0; Mismatches 102;
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les 216; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTCAAGCTGAATGTGGAGGAGCGCCATGGTGGGGCCCCTTACCCGGAAGGGCTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAAGATCGACATCGCCCCTGACGAGATCACGGTCAGCAGTGACTTCGAGGCTCGCA 414
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ROVAX56 3'
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On Jan 19, 1998 th
Contact: Lee, NH
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Eutheria; Rodentia; Sciurognathi; Muridae; M
1 (bases 1 to 473)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M.,
Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                 The Institute for Genomic Research 9712, Medical Center Drive, Rockvij Tel: (301)-838-3529 Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                           AI011632
AI011632.1
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                                                                                                                           primer: M13-21.
           116
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                         1. .473
/organism="Rattus sp."
/db_xref="ATCC (inhost):2021828"
/db_xref="taxon:10118"
/clone="ROVAX56"
/clone_lib="Normalized rat ovary,
/cota="Organ: ovary; Vector: pT7T:
                                                                                                                                      nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                               83 Normalized rat ovary, 3' end, mRNA sequence.
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     /note="Organ: ovary;
Site_2: NotI"
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                       rat ovary, Bento Sources ector: pT7T3Pac; Site_1:
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                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
Insert Size: 1695
High quality sequence stops: 337 Source: IMAGE Consortium,
This clone is available royalty-free through LLNL; contact
IMAGE Consortium (info@image.llnl.gov) for further informat
Insert Length: 1695
Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Sep 21, 1992 this sequence version Contact: Wilson RK
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1 (bases 1 to 402)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,
Parsons,J., Rifkin,L., Rohlling,T., Soares,M., Tan,F.,
Parsyskis,E., Waterston,R., Williamson,A., Wohldmann,P. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-Merck EST Project 
Unpublished (1995)
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/clone_lib="Soares infant
/sex="female"
/dev_stage="73 days post n
                                                                        /db_xref="taxon:9606"
/clone="IMAGE:29543"
                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:401890"
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Pred. No. 9.2e-28;
0; Mismatches 142
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                                                                                                             Unpublished (1996)
On Jan 19, 1998 this sequence version repl
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 406)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI325344 406 bp mRNA EST 23-DEC-1998 mi01c02.y1 Soares mouse placenta 4NbMPl3.5 14.5 Mus musculus clone IMAGE:459170 5' similar to gb:U07634 Mus musculus receptor-protein tyrosine kinase (MOUSE);, mRNA sequence. AI325344
                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
Mus musculus
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Pred. No. 1.2e-24;
0; Mismatches 84
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sequenced mouse its original sel
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Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agattgacaccattgcagctgatgaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgagaacaaactgggtccccaggaactcagctcagaagatttatgtggagctcaagttca 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTACTATGCAGAGTCAGATGTGGACTATGGCACCAACTTCCAGAAGCGCCAGTTCACCA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgtactacatggagtctgatgatgatcatggggtgaaatttcgagagcatcagtttacaa 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCGCACCAACTGGGTGTACCGGGAGGAGGCCGAGCGCATCTTTATTGAGCTCAAGTTCA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATGCCTATCTACATGTACTCGGTGTGCAACGTGGTATCCGGCGACCAGGACAACTGGC
                                                                                                                                                                                                                                                                                                                                                                                      ..., 24123 366 bp mRNA EST 21-JAN-1997 mi01c02.rl Soares mouse placenta 4NbMp13.5 14.5 Mus musculus clone IMAGE:459170 5' similar to gb:U07634 Mus musculus receptor-protein tyrosine kinase (MOUSE);, mRNA sequence. AA024123 AA024123.1 GI:1489009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATTGACACCATCGCCCCTGACGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGTGCGAGACTGTAACAGCTTCCCGGGTGGCGCCAGCTCATGCAAAGAGACCTTCAACC 111
                                                         werser, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 366)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubug Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Gehsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Martin,J., Morris,M., Gehsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Martin,J., Morris,M., Martin,J., Morris,M., Martin,J., Morris,M., Martin,J., Morris,M., Gehsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Martin,M., M., Martin,M., M
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Seq primer: -40RP fr
Unpublished
                                                                                                                                                                                                                                                                                                                             Mus musculus
                                 The WashU-HHMI Mouse
                                                                                                                                                                                                                                                                                                                                                                  house mouse.
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117 c 109 g 100 t 1 others
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/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco
lst strand cDNA was primed with a Not I - oligo(dT) pr
[5'
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459170"
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/dev_stage="adult"
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/sex="unknown"
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   (1996)
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Pred. No. 5.9e-23;
0; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gibco
                                     Project
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                                                                                                                       DEFINITION
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                                                                                                                                                                                                                        AGATTGACACCATCGCCCCTGACGAGA
                                                                                                                                                                                                                                                                                                                                                                               ctctacgagactgcaatagcattccattggttttaggaacttgcaaggagacattcaacc 211
                                                                                                                                                                                                                                                                                                                                                                                                                            TCCGCACCAACTGGGTGTACCGGGAGGAGGCCGAGCGCATCTTTATTGAGCTCAAGTTCA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATGCCTATCTACATGTACTCGGTGTGCAACGTGGTATCCGGCGACCAGGACAACTGCG 231
                                                                                                                                                                                                                                                                                        TCTACTATGCAGAGTCAGATGTGGACTATGGCACCAACTTCCAGAAGCGCCAGTTCACCA
                                                                                                                                                                                                                                                                                                                                                            CGGTGCGAGACTGTAACAGCTTCCCGGGTGGCGCCAGCTCATGCAAAGAGACCTTCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169;
                                                (HUMAN);, ml
AI249967
AI249967.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 8, 1995 this sequence version replaced Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
Fax: 314 286 1810
                                                                                              AI249967 493 bp mRNA EST 05-NOV-1998 qx47d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004483 3' similar to gb:M59371 TYROSINE-PROTEIN KINASE RECEPTOR ECK PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through IMAGE Consortium (info@image.llnl.gov) for fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -28M13 rev2 from Amersham.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:276058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459170"
/clone_lib="Soares mouse p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

103 c 102 g 92 t
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with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
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/tissue_type="placenta"
/dev_stage="adult"
                                                                                   mRNA
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                                                     GI:3846496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.7%;
                                                                                sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 110.2; DB 2
Pred. No. 5.1e-22;
0; Mismatches 98
                                                                                                                                                                                                                         24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990tgagaacaaact99gtccccaggaactcagctcagaagatttatgtggagctcaagt 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCAAGATTGACACCATTGCGCCCGAT
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                                                                                                                                                                                                                                                         AI323334 348 bp mRNA EST 23-DEC-1990 mi01c02.x1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus clone IMAGE:459170 3' similar to 9b:M59371 TYROSINE-PROTEIN FRECEPTOR ECK PRECURSOR (HUMAN); 9b:U07634 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 348)

1 (bases 1 to 348)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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1 (bases 1 to 493)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                               Mus musculus
                                                                                                                                                                                                                               receptor-protein tyrosine kinase (MOUSE);, mRNA sequence
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Location/Qualifiers
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Site_2: NotI; Cloned unidirectionally. Primer:
Average insert size 1.72 kb. Life Technologies
11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:2004483"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 3.7e-18;
0; Mismatches 99;
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                                                                                                                         AAGATTGACACCATCGC 347
                                                                                                                                            aagattgacaccattgc 287
                                                                                                                                                                                                                 ctgtactacatggagtctgatgatgatcatggggtgaaatttcgagagagcatcagtttaca
                                                                                                                                                                                                                                                           ACGGAGCGAGACTGTAACAGCTTTCTCGAAGGCGCCCAGCTCATGCATAGAGACCTTCAAC
                                                                                                                                                                                                                                                                               actctacgagactgcaatagcattccattggttttaggaacttgcaaggagacattcaac
                                                                                                                                                                                                                                                                                                                            TCCGCACCAACTGGTTGTACCGGGAGGAGGCCTGAGCGCATCTCTATTGAGCTCAAGTTC
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                                                                                                                                                                                          CTCTACTATGCAGAGACAGATGTGGACTATGGCACCAACTTCCAGAAGCGCCAGTTCACC
AI337308 496 bp mRNA EST 18-MAR-1999 tb98b01.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062345 3' similar to SW:EPB2_HUMAN P29323 EPHRIN TYPE-B RECEPTOR 2 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
On Jan 17, 1998 this sequence version replaced gi:2043939.
Contact: Marra M./Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

94 c 93 g 74 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="placenta"
/dev_stage="adult"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459170"
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Pred. No. 5.8e-
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71 GTGGAGATGAAGTTTTCGGTGCGTGACTGCAGCAGCATCCCCAGCGTGCCTGGCTCCTGC 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 agtcaaaacaattggctgagaacaaactgggtccccaggaactcagctcagaagatttat 135
                           actcamatggatcttggggaccgtattctgaagctcamcactgagattaggataggtaggt 363
                                                                                                                                              aaggagacattcaacctgtactacatggagtctgatgatgatcatg------gg 243
                                                                                                                                                                                                                                                                                                                                                                                        gtggagctcaagttcactctacgagactgcaatagcattccattggttttaggaacttgc 195
TCCCAGGTGGACCTGGGTGGCCGTCATGAAAATCAACACCGAGGTGCGGAGCTTCGGA
                                                                                                          CCCAACTGGATGGAGAATCCATGGGTGAAGGTGGATACCATTGCAGCCGAGGAGCTTC 250
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Eukaryota; Metazoa;
Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.D., Ph.D.
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Tissue_Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="colon tumor,
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 8.3e-17;
0; Mismatches 149;
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acagtgaagaatctggctatgtttccagacacggtacccatggactcccagtcc---
                                                      GACATAGGTGCCTGGCCATCCTCTCTCTCCGCATCTACTATAAGAAGTGCCCTGCC 358
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wullf04.x1 NCI_CGAP_GC6 F
similar to SW:EPA8_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
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Unpublished (199
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National Cancer Institute, Cancer Genome Anatomy
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AI967980.1 GI:5764798
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                                                                                                                                                                                                                                 /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1238631, 146964-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled germ
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_GC6"
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                                                                                                                                               13.4%;
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Homo sapiens cDNA clone IMAGE:2516671
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                                                                                    29 attacacacccatcaggacttaccaggtgtgcaatgtcatggaccacaggtcaaaacaatt 88
ggctgagaacaaactgggtccccaggaactcagctcagaagatttatgtggagctcaagt 148
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                                                               ATGACATGCCGATCTACATGTACTCCGTGTGCAACGTGATGTCTGGCGACCAGGACAACT
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                                                                                                                                                     143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
On Mar 16, 1998 this sequence version replaced Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=ILO&t2=ILO-HT0156-
251099-132-a12&t3=1999-10-25&t4=1)
Seq primer: puc 18 forward
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The FAPESP/LICR Human Cancer Genome Pr
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ILO-HT0156-251099-132-a12 HT0156 Homo sapiens cDNA, mRNA
AW366937
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                             þ
                                                                                                                                                                                                                                                                /note-"Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone_lib="HT0156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                       13.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW045268 314 bp. mRNA EST 18-SEP-1999 UI-M-BH1-akn-b-03-0-UI.S1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-akn-b-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Jun 5, 1998 this sequence version Contact: Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MS 20892-9643, USA
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Fax: 301 443 9890
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Bonaldo, M.F., Lenno
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                        //lab_host="blug" in the Technologies)"
//lab_host="blug" in the Technologies)"
//lab_host="blug" in the Technologies) with a modified
//note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S1 ibrary is a subtracted library derived from
NIH_BMAP_M_S1, which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
gangila, pineal gland, striatum, hipoccampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 5,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.

"Mac true-ner unwar uses."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI M-BH1-akn-b-03-0-UI"
/clone_1ib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
                                                                  TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE=olfactory-bulbs
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304 TCTACTA 310
                                                        244 CGGTGCGAGACTGTAACAGCTTCCCGGGTGGCGCCAGCTCATGCANAGAGACCTTCAACC 303
                                                                                                              184 TCCGCACCAACTGGGTGTACCGGGAGGAGGCCGAGCGCATCTTTATTGAGCTCAAGTTCA 243
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                                                                       tgagaacaaactgggtccccaggaactcagctcagaagatttatgtggagctcaagttca 151
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0; Mismatches 70;
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Search completed: May 15, 2000, 11:20:21 Job time: 19144 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB seq
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/GOMB.seq:*
6: /cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
7: /cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
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US-08-72-367A-14
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PCT-US96-00419-1
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Sequence 15, Appli
Sequence 14, Appl
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Sequence 34, Appl
Sequence 100, Appl
Sequence 102, Appl
Sequence 1, Appli
Sequence 16, Appl
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Sequence 61, Appli
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US-08-167-919A-9
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Result No.

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12.1	12.1	12.1	12.1	14.8	17.8	17.8	17.8	17.8	17.8	17.8	18.2	21.0	21.0	25.5	25.5	25.5	28:3
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Sequence 23, Appl	Sequence 5, Appl.	Sequence 23, Appl	Sequence 5, Appli	Sequence 1, Appl.	Sequence 4, Appl	Sequence 3, Appli	Sequence 4, Appli	Sequence 3, Appl	N '	Sequence 2, Appl	Sequence 7, Appli	13,	Sequence 9, Appl	•	Sequence 10, App	Sequence 10, Appl	Sequence 11, App

ALIGNMENTS

nucleic acid	н	••
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CHARACTERISTICS:	SEQ	••
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TELEX: 230 901 SANS UR	н	••
TELEFAX: (516) 742-4366	н	••
TELEPHONE: (516) 742-4343		•• •
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APPLICATION NUMBER: PCT/AU92/00294	₽	••
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FILING DATE: 12-DEC-1991	' =1 5	•• •
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APPLICATION NUMBER: PK6841 (AU)	n 35	
	PRI	• ••
CLASSIFICATION: 435	,	••
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APPLICATION NUMBER: US/08/167,919A	Þ	٠.
LICATION DATA:	CUR	٠.
Patentin	S	٠.
OPERATING SYSTEM: PC-DOS/MS-DOS	0.6	•• •
COMPUTER: TRM PC compatible	a s	٠. ٠
MEDITIM TYPE: Floor Atak	, E	
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71B: 11530	۹ C	٠.,
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Garden City	a	••
00 Garden City Plaza	S	٠.
ADDRESSEE: Scully, Scott, Murphy & Presser	æ	•• •
CORRESPONDENCE ADDRESON: L4	0.00	
INVENTION: 4	1.1.1	
OF INVENTION: A NOVEL	TIT	•••
Wilkinson, David	APP	٠.
	APP	٠.
Wicks, Ian	APP	٠.
Simpson, Ric	APP	••
APPLICANT: Boyd, Andrew W.	APP	•• •
	GENER	•• •
batent No. 5674691	patent	
A-9	9T-80-S	
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Sequence 9, Application US/08715106

Patent No. 6020306

Patent No. 6020306

PAPPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Wicks, Ian
APPLICANT: Wilkinson, David
ITILE OF INVENTION: AND USE THEREOF
ITILE OF INVENTION: AND USE THEREOF
CORRESPONDENCE ADDRESS:
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; LOCATION:
US-08-167-919A-9
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Best Local Similarity
Matches 660; Conserv
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ilarity 100.0%;
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Pred. No. 8.7e-208;
0; Mismatches 0;
Murphy
                                     TYROSINE KINASE
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REGISTRATION NUMBER: 31,346
REFERENCE_DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4346
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pairs
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Best Local S
Matches 660
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APPLICATION NUMBER: 08/167
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PK9992
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: PCT/AU
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DO SOTWARE: Patentin Release #1.
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 400 Garden (CITY: Garden City STATE: New York COUNTRY: U.S.A.
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Local Similarity 100.0%; Pred. No. 8.7e-208;
Local Similarity 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                           9999tgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt
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                                                           GGGGTGAAATTTCGAGAGCATCAGTTTACAAAGATTGACACCATTGCAGCTGATGAAAGT
                                                                                                                       GTTTTAGGAACTTGCAAGGAGACATTCAACCTGTACTACATGGAGTCTGATGATGATCAT
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SYSTEM: PC-DOS/MS-DOS
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US-08-162-809-15
                                             Query Match
Best Local S
Matches 537
                                                                                                                                                                                                                TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 3254 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pasquale, Lieuw ...
APPLICANT: Sajjali, Fereydoun G.
APPLICANT: Sajjali, Fereydoun G.
APPLICANT: Sajjali, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TY
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
ADDRESSEE: TAND FLORES
ADDRESSEE: TAND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application Patent No. 5457048
                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A:
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4370 La Jolla VILL
CITY: San Diego
STATE: California
COUNTRY: United States of
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                               FEATURE:
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                                             Local Similarity hes 537; Conserv
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TOPOLOGY: 11
                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                 NAME/KEY:
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                                              Conservative
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32..2980
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                                           Score 463.2; DB 1;
Pred. No. 6.3e-143;
); Mismatches 123;
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application Patent No. 5981245
GENERAL INFORMATION:
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                              APPLICANT: FOX, GAT M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
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CITY: Thousand Oaks
STATE: California
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ZIP: 91320
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1840 Dehavilland
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                                                                                                                           PatentIn Release #1.0,
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RESULT 5
US-08-702-367A-14
; Sequence 14, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION: FOX, GARY M.
APPLICANT: FOX, GARY M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
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; TYPE: nucle;
; STRANDEDNESS
; TOPOLOGY: 1
; MOLECULE TYPE:
; FEATURE:
; FEATURE:
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Best Local Similarity 69.4
Matches 460; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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Pred. No. 4.7e-98;
0; Mismatches 200;
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; LOCATION:
US-08-702-367A-14
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Best Local Similarity 69.4%;
Matches 460; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
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Pred. No. 4.7e-98;
0; Mismatches 200
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PCT-US95-04681-14
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PCT-US95-04681-14
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATEN:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE:
CLASSIFICATION:
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CITY: Thousand Oaks
STATE: California
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                         GTCATGGGGACTTGCAAGGAGACGTTTAACCTGTACTACTATGAATCAGACAACGACAAA
                                            9ttttaggaacttgcaaggagacattcaacctgtactacatggagtctgatgatgatcat 240
                                                                                               gctcagaagatttatgtggagctcaagttcactctacgagactgcaatagcattccattg
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                                                                                                                                                                                                                                                                       Length 3116;
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US-08-222-616-34
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                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb fl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                           CLASSIFICATION: 530
PROOR APPLICATION NUMBER: PCT/US
APPLICATION NUMBER: PCT/US
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST TITLE OF INVENTION: ANTIBODIES NUMBER OF SEQUENCES: 42
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                REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
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460 Point San Bruno Blvd
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Wood, William I
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; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3348 bases
; YPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: 11near
US-08-222-616-34
                            RESULT 8
PCT-US95-04228-34
; Sequence 34, Application
; GENERAL INFORMATION:
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415/952-9881
         Bennett, Brian D. Goeddel, David
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Pred. No. 4.9e-98;
0; Mismatches 200
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STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-34
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FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-1994
TELEFAX: 415/952-9881
TELEYAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3348 bases
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Best Local Similarity
Matches 460; Conserv
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MEDIUM TYPE: 5.25 inch, 360 Kb fl
COMPUTER: IBM PC compattble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Matthews, William Philoant: Tsai, Siao Papplicant: Wood, William TITLE OF INVENTION: PROVINGHER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 460 Point San Bruno B.
CITY: South San Francisco
STAME: California
COUNTRY: USA
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                                                        GTCATGGGGACTTGCAAGGAGACGTTTAACCTGTACTATGAATCAGACAACGACAAA
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GGGCCATTAAGCAAAAAGGGGTTTTACCTGGCTTTTCAGGATGTGGGGGGCCTGCATCGCC
                 ggtcctgtcaacaagaagggattttatttggcattttcaagatgttggtgcttgtgttgcc
                                                                                                                      GAGCGTTTCATCAGAGAGAACCAGTTTGTCAAAATTGACACCATTGCTGCTGATGAGAGC
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Wood, William I
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RESULT 9
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Patent No. 5843/**
GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al
APPLICANT: MAISONPIERRAND RC
TOTAL OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 100, Application US/08469537A Patent No. 5843749
                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3592 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                        FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Ga
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: USSN 0
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 0
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 0
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                                                                    MOLECULE TYPE:
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                                                                                    TOPOLOGY:
                                                                                                STRANDEDNESS:
                                                                                                                                                                                    TELEFAX: 914-345-7721
                                                                                                                                                                                                                                       NAME: Kempler, Ph.D., Gail REGISTRATION NUMBER: 32,143
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E: DNA
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RESULT 10
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: modified_
LOCATION: 3538
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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456; Conserva
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/label= N
/note= "Whe:
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Sequence 102, Application US/08469537A Patent No. 5843749
GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND ROR TY.

al. ROR TYROSINE

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Best Local Similarity 68.5%;
Matches 454; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
       1028
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NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 476..3493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: unkn
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REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3906 base pairs
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                  ttcactcaaatggatcttggggaccgtattctgaagctcaacactgagattagagaagta
                                                                                         ggggtgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt 300
                                                                                                                                                               gttttaggaacttgcaaggagacattcaacctgtactacatggagtctgatgatgatcat
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TTCACCGAACTTGACCTTGGAGACCGGGTCATGAAGCTGAATACGGAGGTCAGAGATGTA
                                                                                                                                           GGACTGGGGACTTGCAAGGAGACCTTTAACATGTATTATTTTGAGTCGGATGATGAGAAT 967
                                                                                                                                                                                                               GCTTCCAGAATTTTTATTGAACTCAAGTTTACTCTGAGGGATTGCAACAGCCTTCCTGGA 907
                                                                     GGGAGAAATATCAAAGAGAACCAGTACATCAAGATCGATACCATTGCTGCTGATGAGAGC 1027
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Pred. No. 7.7e-95;
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Query Match Best Local Similarity

48.1%;

Score 317.4; DB 2; Pred. No. 7.9e-95;

Length 4165;

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US-08-442-248-1
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US-08-442-248-1
                                                            ATTORNEY/AGENT INFORMATION:
NAME: TOYCHIA, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/922-9881
TELEFAX: 415/922-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBERS.
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FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
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            STRANDEDNESS:
TOPOLOGY: 11
                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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                linear
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RESULT 12
US-08-440-815-1
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 kb floppy di
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               Sequence 1, Application US/08440815
Patent No. 5798448
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TIFLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
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Best Local :
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FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOICHLA, TIMOTHY E.
REGISTRATION NUMBER: 36,70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 920
LECOMMUNICATION INFORMATION INFORMATION INFORMATION TELEPHONE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tgggaagagatcagtggtgtggatgaacattacacaccccatcaggacttaccaggtgtgc
                                  caa
                                                             gtcaacaattctaaggaggaagatcctcccaaggatgtactgcagtacagaaggcgaatgg
                                                                                                                                                                                               tttccagacacggtacccatggactcccagtccc---tggtggaggttagagggtcttgt
                                                                                                                                                                                                                                      CIGGITICIGICCGIGICIACIATAAAAAAIGICCIICIGIAGIIAGACAIIIGGCIGII 1272
                                                                                                                                                                                                                                                      ttggtgtctgtgagagtatacttcaaaaagtgcccatttacagtgaagaatctggctatg
                                                                                                                                                                                                                                                                                               GGACCTCTGAGCAAAAAGGGATTTTATCTTGCTTTCCAAGATGTCGGTGCTTGCATCGCT
                                                                                                                                                                                                                                                                                                                TTCACCGAACTTGACCTTGGAGACCGGGTCATGAAGCTGAATACGGAGGTCAGAGATGTA
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                                     660
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GENERAL INFORMATION:
APPLICANT: ZHOU, RENDING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOL
APPLICANT: T. GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGANI
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THEI
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
CORRESPONDENCE ADDRESS: 14
CORRESPONDENCE ADDRESS:
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US-08-673-789-1
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Best Local Similarity
Matches 454; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4322
LENGTH: 4322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,78
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/1:
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                    121
     241
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STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                   gctcagaagatttatgtggagctcaagttcactctacgagactgcaatagcattccattg 180
                                                                                                                                                                                                          aatgtcatggaccacagtcaaaacaattggctgagaacaaactgggtcccccaggaactca 120
                                                                                                                                                                                                                                                          tgggaagagatcagtggtggatgaacattacacacccatcaggacttaccaggtgtgc 60
                                                           gttttaggaacttgcaaggagacattcaacctgtactacatggagtctgatgatgatcat 240
ggggtgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt 300
                                                                                                                                                                                   AAAGTTATGGAACAGAATCAGAATAATTGGCTGTTGACCAGTTGGATCTCTAACGAAGGT 789
                                    GGACTGGGGACTTGTAAGGAGACATTTAACATGTATTATTTTGAATCAGATGATGAGAAT
                                                                                                           GCTTCCAGAATCTTTATTGAACTCAAGTTTACTTTAAGGGACTGCAACAGCCTTCCTGGA 849
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TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
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Pred. No. 8.1e-95;
0; Mismatches 206;
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RESULT 14
US-08-449-645A-12
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US-08-449-645A-12
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APPLICANT: Fox, G
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 10% CONTY: Thousand Oaks
STATE: California
                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3162 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1210 GTCAACCATTCTGTGACAGATGATCCTCCCAAGATGCATTGCAGTGCTGAAGGGGAGTGG
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                                                                   MOLECULE TYPE:
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                                                    FEATURE:
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              NAME/KEY:
LOCATION:
                                                                              STRANDEDNESS: SIT
                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Amgen Patent Operations/RBW STREET: 1840 Dehavilland Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtcaacaattctaaggaggaagatcctccaaggatgtactgcagtacagaaggcgaatgg
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           1..2976
                                                                   CDNA
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Query Match
Best Local Similarity
Matches 445; Conserv

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RESULT 15
US-08-702-367A-12
Sequence 12, Application US/0870236
Sequence 12, Application US/0870236
Patent No. 5981246
GENERAL INFORMATION:
GENERAL INFORMATION:
FORTING OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Kinases
                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Pate
STREET: 1840 Dehavill
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ttggtgtctgtgagagtatacttcaaaaagtgcccatttacagtgaagaatctggctatg
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 3162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 445; Conserv
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ATTORNEY/AGENT INFORMATION:
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Claim 6; Fig Claim 6; Fig This sequence expressed in 1 tumours of hu and the epith (TK) and/or it production and analogues have cellular respondence 31.	07JAN-1993. 119-JUN-1992; AU 121-JUN-1991; AU 121-DEC-1991; AU (HALL-) HALL IN BOYD AD, Simps WPI: 93-036373/ WPI: 93-036373/ WPI: 93-036373/ III-A4 - is EPH FOTCHING IN mod thorapy etc	misc_feature mat_peptide mat_peptide wo9300425-A.	T 1 Q34513; standar Q34513; Q44513; Q44513; Q44513; Q44513; Q44513; Q44513; Q44513; Q44513; Q54514; Q5514; Q55144; Q55	79.8 79.8 79.8 79.8 48.8 48.8 31.4 31.2
; Fig 1; 58pp; English quence encodes human eged in both pre-B cells of human origin, eg. epithelial tumour HeLd/or its ligands are union and/or function of es have activity in trees have activity in trees ponses such as green 3132 BP; 888 A;	AU029 AU-00 AU-00 INST INST pson 5/04. 6. tyrc PH-EI	re 1723 /*ta /not 160. /*ta /*ta /*ta /*ta /*ta /not /*ta /*ta /not	ard; (fi eque essi: ki epit B;ce	12.1 12.1 12.1 12.1 7.4 7.4 4.8
pp; Engl des humas pre-B ce rigin, e tumour gands ar function function such as such as	1. 2. ICAI War War ike		DNA; 3132 BP. Irst entry) nce. on vector; extracel con vector;	44290 4290 4290 4290 40573 40573 40573 786
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ph/elk-like kinase (HEK) and T cell lines and in lymphoid tumours LK63, L a. This receptor-type t seful as agents in modul pre-B, B and T cells. ansducing signals or in owth and/or differentiat 711 C; 759 G;	WALTER & ELIZA. Wicks I, Wilkinson D reactive with monoclona e, useful for phosphory B and T cell function,	1795 e "Potential transmembrane region" 16 f f f "Purified HEK protein #1" 2679 g purified HEK protein #2"	ry) ry; extracellular domain; human; H re-B; cell; T; tumour; lymphoid; L HELa; receptor-type; thymidine ki response; growth; differentiation; 1/Qualifiers a b b b b l 132 c c c c c c c c c c c c c c c c c c c	Q92641 T18394 T42593 T91235 V90061 V33697 V62177 V62177 V64342 V04445 V43665 V46279
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Query Match 100.0%; Score 660; DB 1; Best Local Similarity 100.0%; Pred. No. 1.4e-209; Matches 660; Conservative 0; Mismatches 0;

Length 3132; Indels

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08-JUN-1995.
07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RE.
Pasquale EB, Sajjadi FG;
WPI; 95-215256/28.
P-PSDB; R75711.
                                                                                                                                   Q90659 stand
Q90659;
11-NOV-1995
Eph-related
Cek4; Eph; p
prognosis; s
Gallus sp.
Disclosure; Page 85-89; 129pp; English.

Probes derived from the EPH-related PTKS Cek4 (090659) and (090650) were used to isolate novel cDNA clones (090652-58, 090661-62) from chicken embryo and embryonic brain librarie Cek4 is highly expressed in the chicken developing brain an
                             cancer.
Disclosure;
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Best Local S
Matches 537
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T02948;
16-APR-1996 (first entry)
EPH-like receptor protein tyrosine ki
EPH-like receptor protein tyrosine ki
human eph-like kinase; therapy; diagr
Homo sapiens.
W09528484-A1.
26-OCT-1995; U04681.
14-APR-1995; U5-229509.
15-APR-1994; US-229509.
(AMGE-) AMGEN INC.
FOX GM.
Ting S. Welche
WPI; 95-373799/48.
P-PSDB; R85091.
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Prodn. 1; Page 57-62; 133pp; English.

CC CDNAs (702946-49) coding for 4 novel human EPH-like receptor protein CC cDNAs (702946-49) coding for 4 novel human EPH-like receptor protein CC tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, CC were isolated from a human foetal brain cDNA library using a directed CC receptor PTKs and EPH-like receptor PTKs. BEK5, HEK7 and HEK8 show CC extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known CC EPH-like receptor. The isolated cDNAs are used for prodn. of CC recombinant HEKs and chimeric receptors, in hybridisation assays, and to detect abnormalities in HEK receptor genes.

Sequence 3116 BP; 859 A; 720 C; 812 G; 725 T;
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04-APR-1995, US-222616.
04-APR-1994; US-222616.
(GETH ) GENENTECH INC.
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WPI; 95-366160/47.
P-PSDB; R85936.
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01-DEC-1998.
06-JUN-1995; US-406247.
17-MAR-1995; US-406247.
26-JUL-1991; US-736559.
28-OCT-1993; US-144992.
06-JUN-1995; US-469537.
(RECE-) RECENERON PHARM INC.
MAISONDIETE PC, Masiakowski P
WPI; 99-044884/04.
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V70208;
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Claim 7;
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The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding prot Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes rat Ehk-2. Sequence 3592 BP; 946 A; 916 C; 894 G; 834 T;
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01-DEC-1998.
06-JUN-1995; 469537.
17-MAR-1995; US-406247.
26-JUL-1991; US-736559.
28-OCTT1993; US-144992.
06-JUN-1995; US-469537.
(REGE-) REGENERON PHARM INC.
MAISONDIETTE PC, MASIAKOWSKI P
WPF; 99-044584/04.
                                                                                                                                                                                                                                       proteins
Claim 5; Fig 22; 194pp; English.
--- ~~~aeant invention describes nucleic acid
                                                                                                                                                                           The present invention describes nucleic acid molecules for ror-1 ror-2, ehk-1 and ehk-2. Also described are the corresponding pro Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes rat Ehk-1. Sequence 3906 BP; 1097 A; 876 C; 990 G; 943 T;
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Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1
neurotrophin activity; trkB; proto-oncogene;
binding protein; BDNF; NT-3; diagnosis; ss.
Rattus sp.

Location/Qualifiers
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Key
476. .3493
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or-2; Ehk-1; Ehk-2;
-oncogene; tyrosine
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             W09613518-A1.
09-MAY-1996.
26-OCT-1995; U14016.
27-OCT-1994; US-330128.
07-JUN-1995; US-486449.
(GETH) GENENTECH INC.
CAYAS IN, W11810W JW;
WPI; 96-239448/24.
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T18893;
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         P-PSDB; R97853
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Example 1; Page 47-49; 75pp; English.

A cDNA clone (T18893) codes for rat REK7 (R97853), an eph-related tyrosine kinase receptor, for which AL-1 (see also W97854) is a ligand. It was isolated using degenerate receptor tyrosine kinase receptor, for which AL-1 (see also W97854) is a commerce (T18894-96) to amplify cDNAs of an adult mouse hippocampal cDNA library. A PCR fragment was used as a probe to isolate the full-length REK7 CDNA from a rat hippocampal cDNA library. An CREK-1gG fusion was used to screen cultured cell lines for surface expression of REK7-binding activity. Primers based on isolated ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human foetal brain cDNA library, leading to the isolation of AL-1 cDNA (T18897). Sequence 4165 BP; 1157 A; 907 C; 1035 G; 1066 T;
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Local Similarity 68.5%;
hes 454; Conservative
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                                                                        tttccagacacggtacccatggactcccagtccc---tggtggaggttagaggggtcttgt
                                                                                                                                                                                                                                                                                                           ggtcctgtcaacaagaagggattttatttggcatttcaagatgttggtgcttgtgtgttgcc
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                                                     CTGGTTCCCATCGGGAAATGCATGTGCAAGGCCGGATATGAAGAGAAAAATGGTACCTGT
                                                                                                               GTCAACCATTCTGTGACAGACGATCCTCCCAAAATGCATTGCAGTGCTGAAGGGGAGTGG
                                                                                                                             gtcaacaattotaaggaggaagatoctocaaggatgtactgcagtacagaaggcgaatgg
                                                                                                                                                                       TTCCCTGACACGATCACTGGAGCAGATTCTTCCCAGTTGCTAGAGGTGTCAGGCTCCTGC
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                           660
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Pred. No. 1.7e-95;
D; Mismatches 206;
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RESULT V58192 ID V5

œ

V58192 standard;

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PT with disease

PS Claim 2; Fig 2; 72pp; English.

CC The present sequence encodes mouse Bsk, which is a receptor-like

CC Tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in

CC tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in

CC trom a manual afflicted with a disease, such as neurodegenerative

CC diseases or disorders and neoplasms. The nucleic acid sequence can also

CC be delivered into the limbic system of patients with limbic system

CC neurodegenerative disease, disorder or injury, to promote or enhance

CC limbic system neuron regeneration or growth. Such neurodegenerative

CC diseases include, Chromosomal abnormalities, degenerative growth and

CC injuries, neoplastic conditions, Natheimer's disease, epilepsy,

CC schizophrenia, or stroke and cerebral ischaemia.

SQ Sequence 4322 BP; 1260 A; 887 C; 1055 G; 1120 T;
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Best Local
Matches 45
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29-SEP-1998.
11-JUN-1996; 673789.
04-JAN-1994; US-177812.
11-JUN-1996; US-673789.
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CDS
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Mouse Bsk receptor-like tyrosine kinase cDNA clone.
Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neopla:
Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neopla:
neurodegenerative disease; limbic system neuron regeneration;
chromosomal abnormality; degenerative growth; development disorder;
viral infection; bacterial infection; Alzheimer's disease; epilepsy
schizophrenia; stroke; cerebral ischaemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid sequence encoding protein - used in Bsk nucleic acid probes, used in detecting alterations in level of Bsk messenger-RNA in biological samples isolated from mammal afflicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZHOU/) ZHOU R.
Kromer LF, Schulz NT, Woude WPI; 98-541751/46.
P-PSDB; W71628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KROM/) KROMER L F.
(SCHU/) SCHULZ N T.
(WOUD/) WOUDE G F V.
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25-NOV-1998
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                                                                                                                                                                                                                                    AAAGTTATGGAACAGAATCAGAATAATTGGCTGTTGACCAGTTGGATCTCTAACGAAGGT
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/note= "reco-
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418. .3051
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                                                                                                                                                                                                                                                                                                                                                         Score 317.4; Pred. No. 1.7e

Mismatches
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206;
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Query Match
Best Local
Matches 44
                                                                    Claim 1; Page 49-54; 133pp; English.

CDNAS (T02946-49) coding for 4 novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were isolated from a human foetal brain cDNA library using a directed PCR approach with primers (see T02960-61) based on conserved regions of receptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors. The isolated cDNAs are used for prodn. of recombinant HEKs and chimeric receptors, in hybridisation assays, and to detect abnormalities in HEK receptor genes.

Sequence 3162 BP; 921 A; 667 C; 775 G; 799 T;
                                                                                                                                                                                                                                                                 New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
                                                                                                                                                                                                                                                                                                                            FOX GM,
WPI; 95
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Key
cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T02947 standard; cDNA; 316
T02947;
16-APR-1996 (first entry)
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L5-APR-1994; US-229509
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95-373799/48.
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                Similarity
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45.9%;
nilarity 67.1%;
Conservative
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Score 303; DB 1
Pred. No. 9e-91;
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tgggaagagatcagtggtggatgaacattacacaccccatcaggacttaccaggtgtgc 60

TGGGAAGAGATTGGTGAAGTGGATGAAAATTATGCCCCTATCCACACATACCAAGTATGC

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TRESULT TRESULT TRESULT TO 2949 TO 2949 TO 2940 TO 294
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26-OCT-1995.
14-APR-1995; U04681.
15-APR-1994; US-229509.
(AMGE-) AMGEN INC.
FOX GM, Jing S, Welcher A
WPI; 95-373799/48.
   or prodn.

Claim 1; Page 66-71; 133pp; English.

CDNAs (T02946-49) coding for 4 novel

tyrosine kinases, HEK5, HEK7, HEK8 a

were isolated from a human foetal br
                                                                                                                                                                P-PSDB; R85092.

New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
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T02949;
16-APR-1996 (first entry)
EPH-11ke receptor protein tyrosine kinase HEK11 cDNA.
EPH-11ke receptor protein tyrosine kinase; PTK; HEK11
human eph-11ke kinase; therapy; diagnosis; antibody;
Homo sapiens.
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Mouse developmental kinase 1 MDK1 T2 clone.

Mouse developmental kinase 1; MDK1 T2; receptor tyrosine RTK; signal transduction; probe; diagnosis; gene therapy; neurodegeneration; neuroproliferation; cancer; ss.

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T32962;
11-NOV-1996
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Sequence 4529 BP; 1449 A; 834 C; 1000 G; 1246 T;
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1 (PLAC) MAX PLANCK GES FOERDERUNG WI (SUGE-) SUGEN INC.

Clossek T, Millauer B, HITT-1-1.

WPI; 96-333000
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CDNA cloning using adult mouse brains and Northern blotting identified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that coded for truncated versions (W03422 and W03423; respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1 T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2323 BP; 680 A; 497 C; 609 G; 537 T;
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P-PSDB; W03423.
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Query Match
Best Local Similarity
Matches 452; Conserv

Conservative

45.2%;

Pred. No. 3.4e 0; Mismatches

.4e-89; les 208;

Indels Length

Gaps

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03-JAN-1995; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES F
(SUGE-) SUGEN INC.
C10596k T, M111auer B,
WPI; 96-33988/33.
P-PSDB; W03422.
Example 1; Page 111-12; 128pp; English.

CDNA cloning using adult mouse brains and MDK1 T2 (T32952), that identified 2 clones, MDK1 T1 (T32951) and MDK1 T2 (T32952), that coded for truncated versions (W03422 and W03423, respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32950), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1 T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2901 BP; 890 A; 578 C; 650 G; 783 T;
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Mouse developmental kinase 1; MDK1 T1 clone.
Mouse developmental kinase 1; MDK1 T1; receptor
MTK; signal transduction; probe; diagnosis; ger
neurodegeneration; neuroproliferation; cancer;
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/note= "divergent sequence d'
/note= "divergent sequence d'
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317. .2062
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2031. .
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233. .:
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RESULT
T32960
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11-NOV-1996 (first entry)
Mouse developmental kinase 1 cDNA.
Mouse developmental kinase 1; MDK1; receptor tyrosine kinase;
signal transduction; probe; diagnosis; gene therapy;
signal transduction; neuroproliferation; cancer; ss.
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317.
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3230. .3628
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3627. .4304
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      /note= "alternative 3'-untranslated found in one isolated clone"
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03-JAN-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES F
(SUGE-) SUGEN INC.
Clossek T, Millauer B,
WPI; 96-33398B/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A cDNA clone (T32960) codes for mouse developmental kinase 1 (MDK1) (W03421), a new member of the eck/eph family of receptor tyrosine kinases (RTKS): To isolate the clone, CDNA from mouse embryos was subjected to PCR amplification with primers based on conserved motifs (see also W03426-27) of RTKs. An amplified fragment was used to screen an 11.5-day-old mouse embryo and an adult mouse brain CDNA library to obtain the MDK1 clone. 4 Sequence variants (see also W03422-25) of MDK1 were also identified. MDK1 nucleic acids can be used for the recombinant prodn. of MDK1, as probes to detect MDK1, and for the gene therapy of diseases involving abnormalities in signal transduction, such as neurodegenerative and neuroproliferative disorders and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOERDERUNG
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                                               gaagatcctccaaggatgtactgcagtacagaaggc
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Pred. No. 4.2e-89;
0; Mismatches 208;
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08-JUN-1995:
07-SEP-1994: U10140.
03-DEC-1993: US-162809.
(LJOL-) LA JOLLA CANCER RE.
Pasquale EB, Sajjadi FG;
WPI: 95-215256/28.
P-PSDB: R75714
                                                                                                                                                                                                                                                                                                                                                   variant Cek7+ (Q90661) were isolated from a chick embryo library in lambda gtl1, and another variant, Cek7' (Q90662), from a chick embryonic brain cDNA library in lambda gtl1. The variants may originate via alternative spilcing of the same gene. Cek7 had the lowest level of expression of 7 novel Eph-related kinases examined and was barely detectable in adult tissues.

Sequence 3056 BP; 871 A; 661 C; 762 G; 767 T.
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Claim 2; Page 106-109; 129pp; English.
Novel EPH-related PTK cDNA clone Cek7
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Pred. No. 1.5e-71;
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07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RE
Pasquale EB, Sajjadi FG;
WPI; 95-215256/28.
P-PSDB; R75705.
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Cek7; Eph; protein tyrosine-kinase; prognosis; ss.
Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                       Novel EPH-related PTK cDNA clone Cek7 (given in Q90653) and its variant Cek7+ (Q90661) were isolated from a chick embryo library in lambda gtll, and another variant, Cek7 (Q90662), from a chick embryonic brain cDNA library in lambda gtll. The variants may originate embryonic brain cDNA library in lambda gtll. The variants may originate of expression of 7 novel Eph-related kinases examined and was barely detectable in adult tissues.

Sequence 3059 BP; 860 A; 632 C; 758 G; 809 T;
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Q90653;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. a C O Score Query Match Length 1111 0000 3149 3254 3254 3254 3254 3254 3254 3254 3254 3254 3254 33107 BB 12 MMKIN1 4 DRAJ5030 12 RNU21955 12 RNU21954 4 GGY14271 4 XLSEK1 4 XELPAGAAA 10 HUMRPTKB 10 HSEHK1 10 HSEHK1 41 AC009425 10 HUMRPTK 32 HSJ189K14 32 HSJ189K14 12 555145551111454 NMU58332 000093 000093 014452 014452 0162743 0162743 0162744 0162744 016274 016274 016274 016274 016274 016274 016274 016274 016274 016274 016274 016274 016274 016274 016274 0162744 016274 016274 016274 016274 016274 016274 016274 016 GGCEK7B 2 MMU72207 DRU89295 0 HS61A9 115010 115001 115009 5 AC023783 GGCEK8A CHKCEK4 I15007 CHKCEK8 MMSEK S57168 HUMHEK RNU69278 MUSMEK4SE MUSMEK4 IJ HUMRPTKB HSEHK1 AC009425 HUMRPTK HSJ189K14 MMKIN1T2 U69278 Rattus norv M68515 Mouse eph-r M68514 Chicken eph-r M68514 Gallus gall X6518 M.musculus S57168 Sek-Eph-rel U90033 Human Chrom L36645 Homo sapien AR062743 Sequence AR02348 Sequence AR023488 Sequence AR023488 Sequence AR023488 Sequence M7357 Mus musculu X91191 X.laevis mR L26099 Xenopus lae L36644 Homo sapien AC009425 Homo sapien AC00944 Homo sapien AC00944 Homo sapien AC00944 Homo sapien AC009444 Homo sapien AC009444 Ho A28003 H.sapiens H I68018 Sequence 9 M83941 Human recep Description

ALIGNMENTS

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Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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RKFTSASADVWSYGIVLNEVMSYGERFYREMSNODVIKAVDEGYKLFPPMDCFAALYGL
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Boyd, A.W., Simpson, R. John, Wicks, I.,
Method of screening for ligands to a
Patent: US 5674691-A 9 07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
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Pred. No. 4.7e-190;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3149)
Wicks,I.P., Wilkinson,D., Salvaris,E. and Boyd,A.W.
Molecular cloning of HEK, the gene encoding a receptor
kinase expressed by human lymphoid tumor cell lines
Proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor protein-tyrosine kinase.
Homo sapiens lymphoid tumor cDNA to mRNA.
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891
                               /Godon_start=1
//Godon_start=1
//protein_id="receptor protein kinase"
//protein_id="raha58633.1"
//db_xref="g::183912"
//db_xref="g::183912"
//translation="mcoclsilllscsyldspgeLipopsNeuvnLdskTiogeLGW
//translation="mcoclsilllscsyldspgeLipopsNeuvnLdskTiogeLGW
//translation="mcoclsilllscsyldspgeLipopsNeuvnLdskTiogeLGW
//translation="mcoclsilltscsyldspgeLipopsNeuvnLdskTiogeLGW
//translation="mcoclsilltscsyldspgeNeuvnLangssTomLGDR
ILKLNTEIREVGPVNKGFYLAFODVGACVALVSVRVYEKKCPTVKNLAMFPDTVPM
DSGSLVEVRGSCVNNSKEEDPPRMYCSTEGEMIVPIGKCCNAGYEERGFMCQACRAG
FYKALDGNMKCAKCPHSSTQEBGSMNCRECENNYFRADKDPPSNACTRPPSSPRNVIS
NINETSVILDMSWPLDTGGRKDVTFNIICKKCGWNIKQCEPCSPNVFFLPRQFGLINT
TVTVTDLLAHTNVTFEIDAVNGVSELSSPPQRAAVSITUQAAPSPVLTIKKDRTSR
NSISLSWGEPEHPNGIILDXSVXYYEKGEQETSYTILRARGTNVTISSLKPDTIYVFQ
IRARTAAGYGTNSRKFEFETSPDSFSISGESSQVVMIAISAVAIILLTVVIYVLIGR
FCGYKSKHGADEKRLHFGNHKLIGLERTVDDHTYEDPQAVHEFAKELDATNISID
FCYGKSCHGADEKRLHFGNHKLIGLERTVDDHTYEDPQAVHEFAKELDATNISID
FCYGKSCHGADEKRLHFGNHKLIGLERTVDDHTYEDPGAVATFRGGKTIFIRWTSPEALAY
GYVHRDLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYTTRGGKTIFIRWTSPEALAY
GYVHRDLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYTTRGGKTIFIRWTSPEALAY
RKFTSASDVWYGGIVLMEVMSYGERFYWEMSNODVIKAVDEGYRLPPDMCPAALYQL
MLDCWGKDRNNRPKFEQIVSILDKLIRWFGSLKIITSAAARPSNLLDQSNUDISTFR
TTGDWLMGVRTAHCKEIFTGVEXSSCDTIAKISTDMKKVGVTVVGPQKKIISSIKAL
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                                                                                                                                                                                                                                                                             ttggtgtctgtgagagtatacttcaaaaagtgcccatttacagtgaagaatctggctatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gttttaggaacttgcaaggagacattcaacctgtactacatggagtctgatgatcat 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gctcagaagatttatgtggagctcaagttcactctacgagactgcaatagcattccattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGTCATGGACCACAGTCAAAACAATTGGCTGAGAACAAACTGGGTCCCCAGGAACTCA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aatgtcatggaccacagtcaaaacaattggctgagaacaaactgggtcccccaggaactca 120
                                                                                                                                                                                                                                                                                           gtacccattggcaagtgttcctgcaatgctggctatgaagaagaggttttatgtgccaa 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttcactcaaatggatcttggggaccgtattctgaagctcaacactgagattagagaagta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggggtgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCACTCAAATGGATCTTGGGGACCGTATTCTGAAGCTCAACACTGAGATTAGAGAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGTGAAATTTCGAGAGCATCAGTTTACAAAGATTGACACCATTGCAGCTGATGAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTTTAGGAACTTGCAAGGAGACATTCAACCTGTACTACATGGAGTCTGATGATGATCAT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCAGAAGATTTATGTGGAGCTCAAGTTCACTCTACGAGACTGCAATAGCATTCCATTG
                                                                                Eukaryota; Metazoa; Ch
Eutheria; Rodentia; Sc
1 (bases 1 to 3077)
Li,Y.Y., McTlernan,C.F
                                                                                                                                                                    U69278
U69278.1
2 (bases 1 to 3077)
Li,Y.Y., McTiernan,C.
Direct Submission
                                            Li,Y., McTiernan,C.F. and Feldman,A.M.
IL-1 beta alters the expression of the receptor gene r-EphA3 in neonatal rat cardiomyocytes
Am. J. Physiol. 274 (1), H331-H341 (1998)
                                                                                                                                                                                         RNU69278 3077 bp mRNA Rattus norvegicus eph-related (Rek4) mRNA, complete cds.
                                     98120505
                                                                                                                                 Rattus norvegicus
                                                                                                                                              Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     llarity 100.0%;
Conservative (
                                                                                                                                                                      GI:1943913
                                                                                                      Chordata; Craniata; Ve. Sciurognathi; Muridae;
            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 660; DB 9;
Pred. No. 4.7e-190;
           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
           Feldman, A.M
                                                                                                                                                                                                      receptor
                                                                                                                                                                                                     ROD
tyrosine
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                                                                                                        Vertebrata;
ae; Murinae;
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                                                                                                                                                                                                        kinase
                                                                                                                                                                                                     23-MAR-1998
.nase homolog
                                                                                                        Rattus
                                                                                                                   Mammalia;
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Best Local :
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      421
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                                                                                                                                                                                                                                                                        aatgtcatggaccacagtcaaaacaattggctgagaacaaactgggtccccaggaactca 120
ttggtgtctgtgagagtatacttcaaaaagtgcccatttacagtgaagaatctggctatg
                                                                                                                                         ttcactcaaatggatcttggggaccgtattctgaagctcaacactgagattagagaagta
                                        GGACCAGTCAATAAAAAGGGGTTTTATTTGGCCTTTCAAGATGTTGGTGCTTGTTGCC
                                                             ggtcctgtcaacaagaagggattttattttggcatttcaagatgttggtgcttgtgttgcc
                                                                                                                  TTCACTCAAATGGATCTCGGGGACCGCATTCTAAAACTCAACACTGAGATTAGAGAAGTG
                                                                                                                                                                                              GGTGTCAAATTCCTAGAGCATCAGTTTACAAAGATTGACACCATTGCCGCTGATGAAAGT
                                                                                                                                                                                                                  ggggtgaaatttcgagagagcatcagtttacaaagattgacaccattgcagctgatgaaagt
                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGTCATGGATCACAGCCAAAATAATTGGCTGAGGACAAACTGGGTGCCGAGAAACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGAAGAGCATCAGTGGTGTTGATGAGCATTACACCCAATCAGGACTTACCAGGTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600;
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On Apr 18, 1997 this sequence version replaced g1:1698721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 90.9
00; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  877
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FYKALDGVAKCTKCPPHSSTOEDGSMNCRCENNYFRAEKDPPSARCTRPPSARRNVIS
NIMETSVILDWSWPLDTGGKKDITFNIICKERNYFRAEKDPPSARCTRPPSARRNVIS
TVTUTDLLAHINYTFEIDAINGVSELSSPPROFAVSITINQAAPSPYMIIKKDRTSR
NSISLSWQEPEHPNGIILDYEVKYYEKQEQETSYTILRARGTNVTISSLKPDTTYVFQ
IRARTAGYCTNSRKFEFENSPDSFSISGENSHVMIAISAARTIVLTVVTYVLVGR
FCGYTHSGKGYCTNSRKFEFENSPDSFSISGENSHVDTATAISAAVHEFAKATIAIIAI
DKVVGAGEFGEVCSGRLKFUNGTELFDGLTKTLKVGYTEKQREDFLGEASIMGQFDHPN
IIRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGKKYLSD
INTLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGKKYLSD
INTLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGKKYLSD
INTLEGVALARNILINSNLVCKVSDFGLSRVLEDDFBAAYTTRGGKIPVRWTSPEATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MDCHLSIIILFGCCVLSCSRELSPQPSNEVNLLDSKTIQGELGW
/SYPSHGWEEISGVDEHYTPIRTYQVCKVMDHSQNWLEXIMVPRNSAQKIYVELKFT
LRDCMSIPLYLGTCKEFFULYYMSEDDDHGYKFLEHQFFKIDTIAADESFTQMDLGGK
ILKLNTEIREYGPVNKKGFYLAFQDVGACVALVSYRVYFKKCPFTVKNLAMFPDTVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Rek4"
/codon_start=1
/product="eph-related receptor tyrosine kinase homolog"
/protein_id="AAC06273.1"
/db_xref="GI:1698722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRKFTSASDVWSYGIVLWEYMSYGERPYWEMSNQDVIKAVDEGYRLPLPMDCPAALYQ
LMLDCWQKDRNNRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLLDQSNVDIATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Rek4"
35. .2989
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/dev_stage="neonatal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTTGDWLNGMRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKA
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.3077
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90.9%;
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7.6e-161;
hes 60;
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polyA_signal
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BASE COUNT 578
ORIGIN
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FEATURES
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VERSION
KEYWORDS
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                                                                              Query Match
Best Local
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242 TGGGAAGAGATCAGTGGTGTTGATGAACATTACACACCAATCAGGACTTACCAGGTGTGC 301
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               1 tgggaagagatcagtggtgtgggatgaacattaccaccccatcaggacttaccaggtgtgtg 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tttccagacacggtacccatggactcccagtccctggtggaggttagagggtcttgtgtc
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595; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2032)

Sajjadi.F.G., Pasquale,E.B. and Subramani,S.

Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor

New Biol. 3, 769-778 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete
M68515
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Mouse eph-related
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Mus musculus (strain
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                                                               Conservative
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Tosine kinase.
Thin IRC y
                                                                                                                                                                                                                         /translation="MDCHLSILVLLGCCVLSCSGELSPOPSNEVNLLDSKTIQGELGW
ISYPSHGWEEISGVDEHYTPIRTYQVCNYMDHSQNNWLRTNNWPRNSAQKIYVELKFT
LRDCNSIPLVLGTCKETFNLYYMESDDHGVKFREHOFTK IDTIAADESFTQMDLGDRI
LKLNTEIREVGFVNKKGFYLAFQDVGACVALVSVRVYEKKCFFTVKNLAMFDDTVPMD
SQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPHSSTQEDGSMNCRCENNYFAAEKDPSMACARPPSAPRNVISN
INETSVILDWSWPLDTGEDGSKDITFNIICKKCGMVRQCEPGSPNVRFLPRQLGLTNTT
VTVTDLLAHTNYTFEIDAVNGVSELSSPPQYAAVSITTNQAAPSPVMTIKKDRTSRN
SISLSWQEPEHPNGIILDYEVKYYQKDEQETSYTILRARGTNVTISSLKPDTTYVFQI
SISLSWQEPEHPNGIILDYEVKYYQKDEQETSYTILRARGTNVTISSLKPDTTYVFQI
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                                                                                                                                                                             RARTAAGYGINSRKFEFETSPDCMYYFSF"
2010. .2015
2032
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/codon_start=1
/product="Mek4 secreted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="IRC x Swiss Webster"
/db_xref="taxon:10090"
/dev_stage="11.5 day embryo"
                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA39522.1"
/db_xref="GI:454829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_
                                                                                                                                                             473
                                                                             82.5%;
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                                                            Score 544.8; DB 12;
Pred. No. 5.2e-155;
0; Mismatches 62;
                                                                                                                                                               460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x Swiss Webster) 11.5
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                                                                                            Length 2032;
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Mus.
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••
                                                            Gaps
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VERSION
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                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ma
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 3197)
Sajjadi,F.G., Pasquale,E.B. and Subramani,S.
Identification of a new eph-related receptor tyrosine
from mouse and chicken that is developmentally regulat
encodes at least two forms of the receptor
New Biol. 3, 769-778 (1991)
                                                                                                                                                                                                                     M68513.1 GI:199119
M68513.1 GI:199119
receptor tyrosine kinase.
Mus musculus (strain IRC:
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eph-related
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89. .3040
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1. .3197
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receptor
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SQSLVEVRGSCVNNSKEEDPPRNYCSTEGEWLVPIGKCTCNAGYEERGFICQACRPGF
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767 c 775 g 748 t
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tgggaagagatcagtggtgtggatgaacattacacacccatcaggacttaccaggtgtgc 60 gttttaggaacttgcaaggagacattcaacctgtactacatggagtctgatgatgatcat aatgtcatggaccacagtcaaaacaattggctgagaacaaactgggtccccaggaactca 120 gtacccattggcaagtgttcctgcaatgctggctatgaagaagaggttttatgtgccaa 660 TITCCAGACACAGTGCCCATGGACTCCCCAGTCTTTGGTGGAGGTTAGGGGCTCTTGTGTCTC tttccagacacggtacccatggactcccagtccctggtggaggtttagagggtcttgtgtc ttggtgtctgtgagagtatacttcaaaaagtgcccatttacagtgaagaatctggctatg TICACTCAGATGGATCTCGGGGATCGCATTCTGAAACTCAACACTGAGATTAGAGAAGTG ttcactcaaatggatcttggggaccgtattctgaagctcaacactgagattagagaagta 360 ggggtgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt gctcagaagatttatgtggagctcaagttcactctacgagactgcaatagcattccattg TTGGTGTCTGTGAGAGTGTACTTCAAAAAGTGCCCGTTTACAGTGAAGAATCTGGCTATG GGCGTCAAATTCCGAGAGCATCAGTTCACGAAGATTGACACCATTGCCGCTGATGAAAGT GTTTTGGGGACTTGCAAGGAGACCTTTAACCTGTACTACATGGAGTC---TGATGATCAT GCTCAGAAGATCTATGTGGAGCTAAAGTTCACACTGCGGGACTGTAACAGCATTCCATTG AATGTCATGGATCACAGCCAAAATAATTGGCTGAGGACAAACTGGGGTACCCAGAAACTCA Similarity Conservative 82.5%; 9 Score 544.8; DB 12; Pred. No. 5.3e-155; 0; Mismatches 62; Indels Length ω --Gaps 240 361 421 180 301 778 540 538 300 478 ۲

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                                                             aatgtcatggaccacagtcaaaacaattggctgagaacaaactgggtccccaggaactca 120
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GCGCAGAAGATATATGTGGAGCTCAAGTTTACCTTGAGGGACTGCAATAGTATCCCTCTA
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                                                AATGTTATGGATCACAGTCAAAACAATTGGCTGCGAACAAACTGGATTCCACGCAATTCA
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Chicken eph-related receptor tyrosine kinas
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M68514
M68514.1 GI:454809
M68514.1 GI:454809
receptor tyrosine kinase.
Gallus gallus 10 day embryo embryo cDNA to
Gallus gallus
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Sajjadi,F.G., Pasquale,E.B. and Subramani,S.
Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor
New Biol. 3, 769-778 (1991)
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Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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32. .2
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/codon_start=1
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Pred. No. 1.2e-130;
0; Mismatches 122;
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1 (bases 1 to 3254)
Pasquale, E.B. and Sajj
Eph-related tyrosine )
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I15007
I15007.1 GI
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1. .3254
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                                                                                                                                                                                                                      Direct Submission
Submitted (09-SEP-1994) to the DDBJ/EMBL/GenBank databases.
Kunimasa Ohta, Kumamoto University Graduate School of Medical Sciences, Dept. of Neuroscience and Immunology; 4-24-1 Kuhonj: Kumamoto, Kum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohta, K., Nakamura, M., Hirokawa, K., Tanaka, S., Iwama, A., Suda. Ando, M. and Tanaka, H. The receptor tyrosine kinase, Cek8, is transiently expressed
                                                                                                                                                                                                                                                                                                                                                                  Ohta, K.
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                                                                                                                   /organism="Gallus gallus"
/db_xref="taxon:9031"
/tissue_type="spinal cord"
    /codon_start=1
/product="Cek8"
/protein_id="BAA07373.1"
/db_xref="GI:1236733"
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WIASPLEGGREEVS IMEKNIPLITYCYCCAVTGSRVYPANEVTLLDSRSVQGELG
WIASPLEGGREEVS IMEKNIPLITYCYCUNWEPSONNWIRTDWIPREGAORVIEIK
FTLRDCNSLPGYMGTCKETFNLYYESNDKERFIRESOFAKIDITAADESFTQVDIG
DRIMKLNTEVROVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRRLAQFPDTI
TGADTSSLVEVRAGSCVNNSEEKDVPKMYCGADGEMLVPIGNCLCNAGYEDERNGECOAC
KIGYYKALSTDVACAKCPPHSYSIWEGSTSCTCDRGFFRAENDAASMPCTRPPSAPON
LISNVNETSVNLEWSAPONKGGADDISYNVVCKRCGAGEPSHCKSCGSGYHFSPOONG
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SYSDWLQAIKMERYKDNFTAAGYTTLEAVYHNNQDDLARIGITAITHQNKILSSVQAM
RSQMQQMHGRMVPV"
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hes 468; 162 TGGGAGGAAGTGAGCATAATGGATGAGAAGAACACTCCGATCCGCACCTACCAAGTTTGC 221 1 tgggaagagatcagtggtgtggatgaacattacacacccatcaggacttaccaggtgtgc 60 Similarity 70.0 68; Conservative 51.5%; 0 Score 339.8; DB 4; Pred. No. 1.3e-92; 0; Mismatches 192; Length Indels Ψ Gaps ۳

aatgtcatggaccacagtcaaaacaattggctgagaacaaactgggtcccccaggaactca 120 gttttaggaacttgcaaggagacattcaacctgtactacatggagtctgatgatgatcat GCTCAGAGGGTATATATTGAAATCAAGTTCACGCTGAGAGACTGCCAACAGCCTGCCAGGT 341 GTCATGGGAACTTGCAAAGAGACTTTCAACCTCTATTACTATGAATCAAACAACGACAAG 401 281 240

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2 (bases 1 to 4242)
3 (stardi-Hebenstreit, P., Nieto, M.A., Frain, M., Ma Chestier, A., Wilkinson, D.G. and Charnay, P.
An Eph-related receptor protein tyrosine kinase expressed in the developing mouse hindbrain oncogene 7 (12), 2499-2506 (1992)
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M.musculus mRNA for tyrosine
X65138 S51422
X65138.1 GI:54083
Sek gene; Tyrosine kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 4242)
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DRINKINTEIRDVGPLSKKGFYLAFQDVGACTALVSVRYFYKCPLTVRKLAGFPDTI
TGADTSSILVEVRGSCVUNISEREKDYFKNCGADEFYKRCPLTVRKLAGFPDTI
TGADTSSILVEVRGSCVUNISEREKDYFKNCGADEFYKRCPTRFSAPIN
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LISHVNETSVHLEWSSPQNTGGRODISYNVCKKCGADEFYTTTNQAAPSSIALVQAK
EVTRYSVALAWLEPDRPNGVILEYEVKYYEKDQNERSYRIVTTANAAPSSIALVQAK
EVTRYSVALAWLEPDRPNGVILEYEVKYYEKDQNERSYRIVTTARARTDIKGLNELIA
YVEHYRARTAAGYGDESEPLEVYTNTVEFRITEDPNQAVREFAKEIDASCIKIE
KVIGYGEFGEVCSGRLEVYGKREICVALKTIKAGYTDKQRDFLSEASINGQEDHFNI
IHLEGVVTKCKPVNIITEYMENGSLDAFLRKNDGRFTVLOLVGMLRGIGSGMKYLSDM
SYVHRDLAARNILVNSNLVCKVSDFGMSRVLEDDFAAYTTRGGKIPIRWTAPEALAY
RKFTSASDVWSYGIIVMEVMSVGERFYNDMSNQDVIKALEEGYRLEPPMCPF IALHOL
MLDCWGKERSDRPKFGQIVNLDKLINPNSLKRTGSESSRPNTALLDPSSPEFSAVV
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/dev_stage="8.5 days"
/map="band C"
58. .3018
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/codon_start=1
/product="tyrosine kinase
/protein_id="CAA46268.1"
/db_xref="GI:54084"
2392. .2394
/gene="Sek"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SWISS-PROT: Q03137"
/translation="MAGIFYFILFSFLFGICDAVTGSRYYPANEVTLLDSRSYQGELG
WIASPLEGGWEEVSIMDEKNTPIRTYQVCNYMEASQNNWLRTDWITREGAQRVYIEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Sek"
58. .3018
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2392. .2394
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/strain="C57BL"
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                                                                                  /gene="Sek"
103. .3015
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Best Local Similarity 69.7
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S57168.1
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Gilardi-Hebenstreit,P., Nieto,M.A., Frain,M.,
Chestier,A., Wilkinson,D.G. and Charnay,P.
                                                                                                                                           S57168 4242 bp n
Sek-Eph-related receptor
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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                                                                           TGGGAGGAAGTGAGCATTATGGATGAGAAAAATACACCGATCCGAACCTACCAGGTGTGC
TTCACGCAGGTGGACATTGGTGACCGAATCATGAAACTCAACACTGAGATCCGGGATGTA
                    ttcactcaaatggatcttggggaccgtattctgaagctcaacactgagattagagaagta 360
                                                                                               9999tgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt
                                                                                                                                                      GTCATGGGGACTTGCAAGGAGACGTTTAACCTCTACTATGAGTCGGACAACGACAAG
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                                                                                                                                                                                                                                                     gctcagaagatttatgtggagctcaagttcactctacgagactgcaatagcattccattg
                                                                                                                                                                                                                                                                                                            GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 127779) from the original journal article.
This sequence comes from Fig. 5.
*ERRATUM* Gilardi-Hebenstreit et al., Oncogene (1992)7, 2499-2507.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain Oncogene 8 (4), 1103 (1993)
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KIGYYKALSTDASCAKCPHBYSVWEGATSCTCDRFFFADNDAASMPCTRPESAPLN
LISHVNETSVNLEWSSPQNTGGRODISYNVCKKCGAGDPSKCRPCGSGVHYTPQONG
LKTTRVSITDLLAHTNYTEINAVNGVSKYNPSSPQSVSVTVTTNQAAPSSIALYQAK
EVTRKSTVALAWLEPDRPNGVILLEYEVKXYEKDQNERSYRLYRTAARNTDIKGLNPLTS
YVEHVRARTAAGYGDFSEPLEVTTNITVPSRIIGDGRANSTVLLVSVSGSVLVVILIAA
FVISRRSKYSKAKQEADEEKHLNQGVRTYDDFTYEDDNQAVREFAKEIDASCIKIE
KVIGVGEFGEVCSGLLKVPGKREICVAIKTLKAGYTDKORDFLSEASIMGQFDHPNI
IHLEGVYTKCKPVMIITEYMENGSLDAFLRKNDGFFTYQDLVGMLRGIGSGMKYLSDM
SYVHRDLAARNILVNSHLVCKVSDFGKSRVLEDDPEAAYTTRGGRIPIRFWTAPBAIAY
RKTTSASDVWSYGIVMMLDKIIRPNSLKRTGSESSRPNTALLDESSPEFSAVV
SVGDWLQAIKNDRYKNNFTAAGYTTLEAVVHMSQDDLARIGITAITHQNKILSSVQAM
RTONQQMHGRMVPV"
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/db_xref="taxon:10095"
58. .3018
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FTLRDCNSLPGVMGTCKETFNLYYYESDNDKERFIRESQFGKTDTIAADESFTQVDIG
DRIMKLNTEIRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRNLAQFPDTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Eph-related receptor protein tyrosine kinase; *ERRATUM* Gilardi-Hebenstreit et al., Oncogene (1992) 2499-2507; This sequence comes from Fig. 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MAGIFYFILFSFLFGICDAVTGSRVYPANEVTLLDSRSVQGELG/
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/db_xref="GI:298688"
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58. .3018
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U58332
U58332.1 GI:
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19104-6082, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning of m-ehk2 from the murine inner ear, an tyrosine kinase expressed in the developing and DNA Cell Biol. 15 (10), 817-825 (1996)
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,A.M., Ichimiya,S.,
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/translation="mgg/evrefil/proffflultawtgdcshysnqvylldttvmg
elgwktyflungwaitemdehnreihtyqvcnymephqnnwletnwaisrdaagkiyve
mkrtyflungwisipwliggyckethreihlyyiesdeshtkprygqyikidtiaadesftqmd
Lgdrilklnteirevgpierkgfylyiiesdeshtavyvryfkkcpftyardesftqmd
fiprvdssslupyrgscyksaeerdfpklycgadgmluvplarcigstgyeeleggch
plyrvdssslupyrgscyksaeerdfpklycgadgmluvplarcigstgyeeleggch
Acrpgfykafagntkcskcpphsstyvveatsvchcekgyfraekdppsmactrpppsap
rnvafninetalliemsppsdtggrkdltysvlckkcgldtycedcggclreiprhf
glinnsvvvldpyshunytfeieamngvseljsfrptaltytdbdapsligmark
Dabsonslatsmoapaesngaildyetkytekebgltysfraekdppstlyulff
fylfhirvatatgysgysgkfeerddbtsdmakabgogilvtatavavgeftllytlif
ffelitgrogwyikakmkseekkrhtlonghlrepgittyjdddysdpslahhefake
                                                                                                                                                                                                               /product="receptor tyrosine kinase"
/protein_id="AAB53836.1"
/db_xref="GI:1457961"
                                                                                                                                                                                                                                                                                        /note="eph-related tyrosine kinase; simil
norvegicus receptor-like tyrosine kinase
Accession Number S51605"
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="Balb/c"
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PAGRPVMIVVEYMENGSLDSFLRKHDGHFTVIQLVGMLRGIASGKYTKLSDMGYVHRDL
AARNILVNSNLYCKVSDFGLSRYLEDDPEAAYTTTGGKIPIIRWTAPEALAXKKYSSAS
DAWSYGIVMWEVMSYGERPYWEMSNQDVILSIEEGYRLPAPMGCPPSLQQLMLHCWQK
ERNHRRKFTDIVSFLDKLIRNESALHTLVEDILVMPESFGDVFEYPLFVTVGGMLDSI
KMGQYKSNFMAAGFTTFDLISRMSIDDIRRIGVILIGHQRRIVSSIQTLRHMMHIQE
KGFHY"
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Direct Submission

Submitted (14-FEB-1997) Informatics, Southwestern Medical Center,

5323 Harry Hines, Dallas, TX 75235-8591, USA

3 (bases 1 to 77197)

Evans,G.A., Bradbury,P., Brignac,S., Bumeister,R., Burbee,D.,

Davie,J., Davies,C.J., Davis,C., English,C., Fondon,T.,

Franklin,T.L., Garner,H.R., Gordon,M., Gotway,G., Grant,O.,

Hahner,L., Harris,J., Hinson,S., Megarity,C., Narayanaswamy,U.,

Newton,J., O'Brien,K., Oliver,T., Patel,P., Probst,S., Rayner,S.,

Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D.,

Ward,T. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Direct Submission

Submitted (06-AUG-1997) Genome Science and Technology Center, University of Texas Southwestern Medical Center at Dallas, 53 Harry Hines Blvd, Dallas, TX 75235-8591, USA

On Jun 19, 1997 this sequence version replaced g1:1890102.

Location/Qualifiers
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1 (bases 1 to 77197)

Evans.G.A., Bradbury,P., Brignac,S., Bumeister,R., Burbee,D.,
Davie,J., Davies,C.J., Davis,C., English,C., Fondon,T.,
Pranklin,T.L., Garner,H.R., Gordon,M., Gotway,G., Grant,O.,
Hahner,L., Harris,J., Hinson,S., Megarity,C., Narayanaswamy,U.,
Newton,J., O'Brien,K., Oliver,T., Patel,P., Probst,S., Rayner,S.,
Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D.,
Mard,T. and Wilson,R.
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/rpt_family="MER25"
complement(35627. .36574)
/rpt_family="LTR13"
complement(40418. .40703)
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complement(12868. .15221)
/rpt_family="Tigger1"
complement(20435. .20710)
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/clone="pDJ298k13"
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1 (bases 1 to 3107)

Fox,G.M., Holst,P.L., Chute,H.T., Lindberg,R.A., Janssen,A.M., Basu,R. and Welcher,A.A.

CDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine Kinases
Oncogene 10 (5), 897-905 (1995)
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EPH-11ke receptor PTK; receptor protein-tyrosine kinase.
Homo sapiens (clone library: Stratagene premade library, cat
#936206) female fetus, 17-18 weeks gestation brain cDNA to mRNA.
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SVGDWLQAIKMDRYKDNFTAAGYTTLEAVVHVNQEDLARIGITAITHQNKILSSVQAM
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DEFINITION
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Sequence
I44522
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                                        1 (bases 1 to 3348)
Bennett, B.D., Goeddel, D. and Matthews, W.
Protein tyrosine kinase agonist antibodies
Patent: US 5635177-A 34 03-JUN-1997;
                                                                            Unclassified.
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Search completed: May 15, Job time: 18656 sec 2000, 11:43:49

Title: Perfect score: Sequence:

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                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/167,919A
FILING DATE: 18-APP-194
CLASSIFICATION UNMBER: PK6841 (AU)
FILING DATE: 12-JUN-1991
PRIOR APPLICATION NUMBER: PK992 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION NUMBER: PK992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 91.99
ATTORNEY/AGENT NUMBER: 91.99
ATTORNEY/AGENT NUMBER: 91.99
ATTORNEY/AGENT NUMBER: 91.99
TELECOMMUNICATION LONGER: 91.99
TELECOMMUNICA
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APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Walkinson, David
TITLE OF INVENTION: A NOVEL RE
TITLE OF INVENTION: AND USE TH
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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TYPE:
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US-08-162-809-18

US-08-162-809-12

US-08-449-045A-11

US-08-702-367A-11

PCT-US95-04681-11

US-08-673-789-6

US-08-162-809-2

US-08-162-809-2

US-08-162-809-1

US-08-162-809-1

US-08-162-809-1

US-08-162-809-14

US-08-162-809-14

US-08-162-809-14

US-08-162-809-14

US-08-162-809-14

US-08-162-809-14

US-08-162-809-14

US-08-162-809-14

US-08-449-645A-20

PCT-US95-04681-20

US-08-449-645A-18
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Result No.

Score

1132 914.5 914.5 914.5 905.5 905.5 905.5 905.5 905.5 905.5 8866.5 8866.5 8866.5 8860.5 8860.5 8860.5 8860.5 8860.5

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                                                                                                                              Query Match
Best Local S
Matches 220
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Best Local Similarity
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APPLICANT: Fox, G
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: [
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                    Local 220;
      112
232
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                                                            52 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 111
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CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDIGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                        TYPE:
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                                                                             1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIVVELKFTLRDCNSIPL 60
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                                                                                                                             h 100.0%; Score 1200; DB 2; Similarity 100.0%; Pred. No. 3.7e-122; 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                        amino acid
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Pred. No. 3.7e-122;
); Mismatches 0;
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RESULT 4
US-08-715-106-10
; Sequence 10, Application US/08715106
; Patent No. 6020306.
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-367A-21
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Best Local Similarity
Matches 220; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
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CLASSIFICATION: 435
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CITY: Thousand Oaks
STATE: California
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ZIP: 91320
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                                                                                                                                                                                                                                                                                                                  1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                    NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                  GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV
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IBM PC compatible
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40 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1200; DB 2; 100.0%; Pred. No. 3.7e-122; tive 0; Mismatches 0;
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Best Local
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FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/167,919
FILING DATE: 18-APPR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PK9992 (AU)
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/AU92/0029-
FILING DATE: 19-JUN-1992
ATTORNEY/ACENT INFORMATION:
NAME: DIGIGILO: FFARK'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LENGTH: 983 amino acid
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APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
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                                                                      112 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                  181 NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                         VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 271
                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 1200; DB 3; ilarity 100.0%; Pred. No. 3.7e-122; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                      Length 983;
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                                                                                                                              : Sequence 16, Application US/08162809
: Patent No. 5457048
: GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 220; Conserv
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: PCT/US95/04681
                                  CORRESPONDENCE ADDRESS:
                                                               APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYRE
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES,
                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: EPH-Lik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                    232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                                                                                                                                                                                        GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV 180
                                                                                                                                                                                                                                                                          NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
                                                                                                                                                                                                                                                                                                         GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV
                                                                                                                                                                                                                                            NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 271
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California
4370 La
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1200; DB 4; ilarity 100.0%; Pred. No. 3.7e-122; Conservative 0; Mismatches 0;
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                  CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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 Jolla Village Drive,
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                                                                               TYROSINE KINASES
   Suite 700
                                                                AND METHODS
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                                                                OF USE
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Sequence 4, Application US/08673789
Patent No. 5814479
GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING; SCHULZ,
APPLICANT: T: KROMER, LAWRENCE,
APPLICANT: GEORGE, F:
APPLICANT: OF INVENTION: BSK RECEPTOR:
TITLE OF INVENTION: TYROSINE KINA-
TITLE OF INVENTION: USE IN DIAGNO.
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 983 amino acids;
TYPE: amino acid;
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-809-16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 91,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                             COUNTRY: US
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 WEEISGVDEHYTPIRTYQESNVMDHSQNNWLRTNWIPRNSAQKIYVELKFTLRDCNSIPL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
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                                                                                                               NEW YORK
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: United States
                                                                                                                                                        345 PARK AVENUE
                                                                                               USA
                                                                                                                                                                                                                                                                                                                              ZHOU, RENPING; SCHULZ, NICHOLAS,
T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                            MORGAN & FINNEGAN
                                                                                                                                                                                                                               TYROSINE KINASE AND LIGAND AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.7%;
94.1%;
                                                                                                                                                                                                                                                                                           BSK RECEPTOR LIKE
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Pred. No. 3.5e-115;
7; Mismatches 6;
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Best Local Similarity 94.1%;
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08673789 Patent No. 5814479
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,

APPLICANT: T:; KROMER, LAWRENCE, F:; VANDE WOUDE,

APPLICANT: GEORGE, F.

TITLE OF INVENTION: BSK RECEPTOR LIKE

TITLE OF INVENTION: TROSINE KINASE AND LIGAND AND THEIR

TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 14
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INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
TELEFAX: 4377-7
                                                                                             ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
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FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,:
                 COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
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LENGTH: 982
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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STRANDEDNESS: UNI
                                                                                                                                               COUNTRY: U
ZIP: 10154
                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 WEETSGVDENYTPIRTYQESNVMDHSQNNWLRTNWIPRNSAQKIYVELKFTLRDCNSIPL 110
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                                                                                                                                                                                                                                                   ADDRESSEE:
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  APPLICATION
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                                                                                                                                                                                      NEW YORK
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                                                                                                                                                                     USA
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Pred. No. 9.5e-115;
7; Mismatches 6;
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FILING DATE: CLASSIFICATION:

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US-08-469-537A-101
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REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 164; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 101, Application US/08469537A Patent No. 5843749
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
NAME: TORNITON NUMBER: 37,341
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Maisonpi
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER: 08/1
FILING DATE: 04-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
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                                                                                                                                                                                                                                                                                                    STREET: 777 Old CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
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                                                                                                                                                                                                                                                                                                                                                                                             Maisonpierre, et al.
VENTION: EHK AND ROR TYROSINE
VENTION: KINASES
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                                                                                                                                                                                                                                                                                                                                                                                    107
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US-08-449-645A-15
; Sequence 15, Application US/08449645A
; Patent No. 5981245
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SEQUENCE CHARACTERISTICS:
LENGTH: 948 amino acids
TYPE: amino acid
                              REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION: 914-345-7400
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NAME: Kempler, Ph.D., Gail
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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REGISTRATION NUMBER: 32,143
                                                                                                                         FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                              CITY: Thousand Oaks
STATE: California
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Local Similarity 74.0%;
nes 159; Conservative 3:
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amino acid
         986 amino acids
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1840 Dehavilland Drive
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26-JUL-1991
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;; Pred. No. 4.4e-91;
31; Mismatches 24
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114 VMGTCKETFNLYYYESDNDKERFIRENQFVKIDTIAADESFTQVDIGDRIMKLNTEIRDV 173

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; MOLECULE TYPE:
US-08-449-645A-15
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                                                                                                                                                                                   ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-702-367A-15
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US-08-702-367A-15
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GENERAL INFORMATION:
APPLICANT: Fox, G
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Best Local :
                                                                                                             Matches
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                         RÈFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 986 amino acids
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 104v CITY: Thousand Oaks
STATE: California
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TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                             WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
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                  VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                               WEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPG 113
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1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fox, Gary M.
                                                                                                         75.5%; Score 905.5; DB 2; llarity 73.3%; Pred. No. 4.5e-90; Conservative 30; Mismatches 28;
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73.3%;
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DB 2;
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   GENERAL INFORMATION:
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RESULT 13
US-08-222-616-36
Sequence 36, Application
Patent No. 5635177
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PCT-US95-04681-15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY: 1320
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOWNITER: IBM PC compatible
TOWNITER: TOWNEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0468
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Lik
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Amgen Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                   180 VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
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                                                                                                                                                                                                                                                                                        61 VLGTCKETFNLYYMESDDDHGVKFREHOFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                            54 WEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Winter, Robert
                                                                                                                                                                                                                                                                                                                                                                  1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                               GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                                                                                                                                    VMGTCKETFNLYYYESDNDKERFIRENQFVKIDTIAADESFTQVDIGDRIMKLNTEIRDV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ
                                                                                                                                                                                          GPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSC
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                                                                                                                 VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                         75.5%;
73.3%;
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                       US/08222616
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Pred. No. 4.5e-90;
""Amatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version
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                                                                                                                 274
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APPLICANT:

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RESULT 14
PCT-US95-04228-36
; Sequence 36, Application PC/TUS9504228
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
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Best Local Similarity 73.3
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/Provers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino aci
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US93/00586 FILING DATE: 22-JAN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                         180
                                                                                                                                                                       174
                                                                                                                                                                                                                                114
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                           VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
                                                                                                                                                                  GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC 179
                                                                                                            VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ 274
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Goeddel,
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Wood, William I
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David
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Pred. No. 5.2e-90;
0; Mismatches 28;
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RESULT 15
US-08-673-789-2
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APPLICATION UNMEER: 08/222616

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Wendy M. Lee

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 821P

TELECOMMUNICATION INFORMATION:

TELEPIONE: 415/225-1994

TELEPIX: 415/225-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 36:
   GENERAL INFORMATION:
APPLICANT: ZHOU, R
APPLICANT: T.; KRO
APPLICANT: GEORGE,
TITLE OF INVENTION:
                                                                                        Sequence 2, Application US/08673789 Patent No. 5814479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                         61 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                                                                                                                                54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162;
                                                                                                                                                                                                VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ
                                                                                                                                                                                                                                                                    GPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSC 233
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T: ZHOU, RENPING; SCHULZ, NICHOLAS,
T: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
T: GEORGE, F.
INVENTION: BSK RECEPTOR LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee, James M.
Matthews, William
Tsai, Siao Ping
Wood, William I.
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Goeddel, David
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73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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Pred. No. 5.2e-90;
30; Mismatches 28
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; LENGTH: 877
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
US-08-673-789-2
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Search completed: May
Job time: 4147 sec
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TITLE OF INVENTION: USE IN DIAGNOSTIC AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/673,789
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELEPAN: (212) 751-6849
TELEPAN: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877
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                                                                                     180 VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
||:| :||:|:|| |||||||||| || ||||:|| ||
265 VNHSVTDDPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ 305
                                                                                                                                                                                                                                      205 GPLSKKGFYLAFQDVGACIALVSVRVYYKKCPSVVRHLAIFPDTITGADSSQLLEVSGSC 264
                                                                                                                                                                                    121, GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC 179
                                                                                                                                                                                                                                                                                                            UNKNOWN
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               2000, 22:25:58
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